GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 12, 2003, 15:28:01 ; Search time 84 Seconds
(without alignments)
591.445 Million cell updates/sec

Title: US-09-807-132-4
Perfect score: 1611
Sequence: 1 MDSLNQTRVTEFVFLGLTDN.....VKSAMKQLRQRQVFFTKSYT 313

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1611	100.0	313	21	AAY90872	Human G protein-co
2	1611	100.0	313	22	AAU10306	G-protein coupled
3	1611	100.0	313	22	AAG72077	Human olfactory re
4	1611	100.0	313	23	ABP95912	Human GPCR polypep
5	1380	85.7	327	22	AAG72705	Murine OR-like pol
6	992	61.6	330	22	AAG72706	Murine OR-like pol
7	985	61.1	335	22	AAG72080	Human olfactory re
8	938	58.2	311	22	AAU24670	Human olfactory re
9	938	58.2	311	22	AAG72291	Human olfactory re
10	938	58.2	311	23	ABP95716	Human GPCR polypep
11	938	58.2	311	23	AAB71364	Human GCREC-43 INC
12	938	58.2	311	23	AAU95650	Human olfactory an
13	938	58.2	311	23	AAU85290	G-coupled olfactor
14	929	57.7	314	22	AAG71471	Human olfactory re
15	929	57.7	314	23	ABP95834	Human GPCR polypep
16	929	57.7	314	23	ABJ04000	Human G-protein co
17	929	57.7	314	23	ABJ04001	Human G-protein co
18	929	57.7	314	23	ABJ04035	Human G-protein co
19	929	57.7	314	23	AAU85337	G-coupled olfactor
20	929	57.7	314	24	ABU11200	Human G-protein co
21	927.5	57.6	310	22	AAU24739	Human olfactory re
22	927.5	57.6	310	22	AAG71915	Human olfactory re
23	927.5	57.6	310	23	ABP95708	Human GPCR polypep
24	927.5	57.6	310	23	ABG76839	Human G-protein co
25	927.5	57.6	310	23	AAU95691	Human olfactory an
26	927.5	57.6	310	23	AAU85359	G-coupled olfactor
27	927.5	57.6	310	24	ABU11155	Human G-protein co
28	927.5	57.6	313	22	AAG71495	Human olfactory re
29	927	57.5	314	22	AAU24717	Human olfactory re
30	919	57.0	322	22	AAG71919	Human olfactory re
31	919	57.0	324	23	ABP61145	Human GPCRX protei
32	919	57.0	324	23	AAU95689	Human olfactory an
33	919	57.0	348	22	AAU24720	Human olfactory re
34	919	57.0	348	23	ABP95924	Human GPCR polypep
35	919	57.0	348	23	AAU85340	G-coupled olfactor
36	917.5	57.0	310	23	ABP51597	Human G protein co
37	911	56.5	325	24	ABU11173	Human G-protein co
38	905	56.2	315	22	AAG71474	Human olfactory re
39	905	56.2	315	23	AAE18262	Human G-protein co
40	905	56.2	325	22	AAU24718	Human olfactory re
41	905	56.2	325	23	ABP95833	Human GPCR polypep
42	905	56.2	325	23	AAU85338	G-coupled olfactor
43	900	55.9	318	22	AAU10320	G-protein coupled
44	900	55.9	318	22	AAU05140	Human odorant rece
45	900	55.9	318	23	AAU95525	Human olfactory an

ALIGNMENTS

RESULT 1
AAY90872
ID AAY90872 standard; Protein; 313 AA.
XX
AC AAY90872;
XX
DT 29-AUG-2000 (first entry)
XX
DE Human G protein-coupled receptor GTAR14-1 SEQ ID NO:4.
XX
KW Human; G protein-coupled receptor; GTAR; olfactory receptor; OR;
KW immune response; haematopoiesis; immunomodulatory; regulation.
XX
OS Homo sapiens.
XX
PN WO200021999-A1.
XX
PD 20-APR-2000.
XX
PF 08-OCT-1999; 99WO-JP05578.
XX
PR 09-OCT-1998; 98JP-0288565.
PR 07-DEC-1998; 98JP-0347546.
PR 21-DEC-1998; 98JP-0363537.
XX
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI Maeda M, Nakata Y, Nomura H;
XX
DR WPI; 2000-317946/27.
DR N-PSDB; AAA38953.
XX

PT Novel G protein-coupled receptor proteins encoded by the olfactory
PT receptor gene family are useful in screening drugs or their ligands to
PT regulate the control of the immune response and hematopoiesis -
XX
PS Claim 1; Page 100-102; 159pp; Japanese.
XX
CC The present sequence represents a G protein-coupled receptor protein
CC designated GTAR14-1, isolated from human, which is functional in the
CC immune response and control of haematopoiesis. The G protein-coupled
CC receptors from the present invention have immunomodulatory and
CC haematopoiesis regulatory activities. The G protein-coupled receptors
CC and nucleotide sequences encoding them can be used in screening drugs
CC or their ligands to regulate the functions of immune response and
CC haematopoiesis control.
XX
SQ Sequence 313 AA;

Query Match 100.0%; Score 1611; DB 21; Length 313;
Best Local Similarity 100.0%; Pred. No. 4.4e-172;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
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Db         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
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Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTC 240
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Db        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTC 240

Qy        241 SAHFMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300
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Db        241 SAHFMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300

Qy        301 LRQRQVFFTKSYT 313
              |||||||||||||
Db        301 LRQRQVFFTKSYT 313
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RESULT 2
AAU10306
ID AAU10306 standard; protein; 313 AA.
XX
AC AAU10306;
XX
DT 25-JAN-2002 (first entry)
XX
DE G-protein coupled receptor (GCREC) #7.
XX
KW G-protein coupled receptor; GCREC; vaccine; gene therapy;
KW cell proliferation disorder; cancer; arteriosclerosis;
KW neurological disorder; epilepsy; stroke; cardiovascular disorder;
KW hypertension; ischaemic heart disease; gastrointestinal disorder;
KW anorexia; peptic ulcer; autoimmune disorder; inflammatory disorder;
KW diabetes; osteoporosis; psoriasis; metabolic disorder; obesity;
KW schizophrenic disorder; neuroskeletal disorder.
XX
OS Homo sapiens.
XX
PN WO200166742-A2.
XX
PD 13-SEP-2001.
XX
PF 01-MAR-2001; 2001WO-US06814.
XX
PR 03-MAR-2000; 2000US-186854P.
PR 10-MAR-2000; 2000US-188384P.
PR 17-MAR-2000; 2000US-190453P.
PR 20-MAR-2000; 2000US-190730P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Lal P, Tang YT, Patterson C, Yao MG, Shih LL, Tribouley CM;
PI Lu DAM, Yue H, Khan FA, Policky JL, Au-Young J, Yang J;
PI Harland L, Walsh RT, Lo TP, Borowsky ML;
XX
DR WPI; 2001-656776/75.
DR N-PSDB; AAS15903.
XX
PT Novel G-protein coupled receptor polypeptides, for treating and
PT preventing autoimmune/inflammatory disorders, neurological disorders,
PT cell proliferative disorders, cardiovascular disorders and viral
PT infections -
XX
PS Claim 1; Page 119; 141pp; English.
XX
CC The invention describes a novel isolated polypeptide, selected from a
CC group of 21 G-protein coupled receptor polypeptides (GCREC) and useful in
CC vaccines and gene therapy. The polypeptide (I) is useful for screening
CC for agonist or antagonist of (I), compounds specifically binding to (I),
CC or compounds that modulate the activity of (I). The polynucleotide
CC encoding (I) is useful for screening a compound for effectiveness in
CC altering expression of a target polynucleotide comprising (II), by
CC exposing a sample comprising the target polynucleotide to a compound,
CC detecting altered expression of the target polynucleotide, and comparing
CC the expression of the target polynucleotide in the presence of varying
CC amounts of compound and in the absence of the compound. (I) and (II) are
CC useful for diagnosis, treatment and prevention of cell proliferative
CC disorders (e.g. cancers, arteriosclerosis, atherosclerosis), neurological
CC disorders (e.g. epilepsy, stroke, schizophrenic disorders and
CC neuroskeletal disorders), cardiovascular disorders (e.g. hypertension,
CC ischaemic heart disease), gastrointestinal disorders (e.g. anorexia,
CC peptic ulcer), autoimmune/inflammatory disorders (e.g. diabetes mellitus,
CC osteoporosis, psoriasis), and metabolic disorders such as obesity.
CC Furthermore, the polynucleotide is useful; as primers for detecting
CC single nucleotide polymorphisms; as elements in microarray, to monitor or
CC measure protein-protein interactions, drug-target interactions, and gene
CC expression profiles; to generate a transcript image of a tissue or cell
CC type, and to generate hybridisation probes useful in mapping the
CC naturally occurring genomic sequence. This is the G-protein coupled
CC receptor 7 (GCREC-7), one of 21 GCREC proteins described in the method of
CC the invention.
XX
SQ Sequence 313 AA;

Query Match 100.0%; Score 1611; DB 22; Length 313;
Best Local Similarity 100.0%; Pred. No. 4.4e-172;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
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Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTC 240
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Qy        301 LRQRQVFFTKSYT 313
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Db        301 LRQRQVFFTKSYT 313
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RESULT 3
AAG72077
ID AAG72077 standard; Protein; 313 AA.
XX
AC AAG72077;
XX
DT 30-JUL-2001 (first entry)
XX
DE Human olfactory receptor polypeptide, SEQ ID NO: 1758.
XX
KW Human; olfactory receptor; OR; primary scent determination;
KW secondary scent determination; polypeptide library; odour receptor;
KW scent profile; scent fingerprint; scent representation.
XX
OS Homo sapiens.
XX
PN WO200127158-A2.
XX
PD 19-APR-2001.
XX
PF 06-OCT-2000; 2000WO-US27582.
XX
PR 08-OCT-1999; 99US-0158615.
PR 24-FEB-2000; 2000US-0184809.
XX
PA (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
XX
DR WPI; 2001-290713/30.
XX
PT New polynucleotides which encode polypeptides involved in olfactory
PT sensation for identifying olfactory agonists and antagonists -
XX
PS Claim 11; Page 1153; 1857pp; English.
XX
CC The present sequence is an olfactory receptor which is encoded by
CC one of a number of novel polynucleotides. The polynucleotides can be
CC used in screening for olfactory agonists and antagonists. The methods
CC allow for the determination of primary scents and the identification
CC of the odour receptors used to detect these primary scents. The methods
CC also enable determination of secondary scents and the identification of
CC combinations of odour receptors that are involved in detecting such
CC secondary scents. This enables the construction of a scent representation
CC (also called a scent fingerprint or scent profile), which may be used to
CC re-create and edit scents. Libraries of olfactory receptors are useful
CC for determining the interaction pattern of a composition with the
CC receptors, and can be used for determining differences in the olfactory
CC faculties of different individuals.
XX
SQ Sequence 313 AA;

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  Query Match             100.0%;  Score 1611;  DB 22;  Length 313;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-172;
  Matches  313;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
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Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
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Db         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
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Db        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTC 240
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Qy        241 SAHFMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300
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Db        241 SAHFMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300

Qy        301 LRQRQVFFTKSYT 313
              |||||||||||||
Db        301 LRQRQVFFTKSYT 313
```

RESULT 4
ABP95912
ID ABP95912 standard; Protein; 313 AA.
XX
AC ABP95912;
XX
DT 06-MAR-2003 (first entry)
XX
DE Human GPCR polypeptide SEQ ID NO 634.
XX
KW Human; GPCR; G protein coupled receptor; signal transduction; olfactory;
KW drug development; gustatory; taste; fragrance; receptor.
XX
OS Homo sapiens.
XX
PN WO200216548-A2.
XX
PD 28-FEB-2002.
XX
PF 30-JUL-2001; 2001WO-IB01446.
XX
PR 04-AUG-2000; 2000JP-0237818.
PR 13-FEB-2001; 2001JP-0034434.
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI Haga T, Takeda S, Mitaku S;
XX
DR WPI; 2002-304118/34.
DR N-PSDB; ABZ43186.
XX
PT Database global search for G protein-coupled receptors, proteins and
PT encoded genes for studying in vivo signal transduction mechanism and
PT identifying targets for drug development -
XX
PS Claim 10; SEQ ID NO 634; 97pp + Sequence Listing; Japanese.
XX
CC The invention relates to a method for screening G protein-coupled
CC receptor (GPCR) genes (ABZ42870-ABZ43216) and/or GPCR proteins
CC (ABP95596-ABP95942) by extracting open-reading frames containing 6-8
CC transmembrane domains with 250-1000 amino acid residues to give a gene
CC homologous with a known GPCR gene. The receptor proteins and encoded
CC genes are useful for studying in vivo signal transduction mechanism and
CC identifying targets for drug development e.g. based on olfactory and
CC gustatory receptors in form of agonists and antagonists by screening
CC intrinsic and extrinsic ligands as bitter taste inhibitors, taste
CC enhancers and fragrance improvers.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 313 AA;

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  Query Match             100.0%;  Score 1611;  DB 23;  Length 313;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-172;
  Matches  313;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        241 SAHFMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300
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Db        241 SAHFMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300

Qy        301 LRQRQVFFTKSYT 313
              |||||||||||||
Db        301 LRQRQVFFTKSYT 313
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RESULT 5
AAG72705
ID AAG72705 standard; Protein; 327 AA.
XX
AC AAG72705;
XX
DT 31-JUL-2001 (first entry)
XX
DE Murine OR-like polypeptide query sequence, SEQ ID NO: 2387.
XX
KW Mouse; olfactory receptor; OR; primary scent determination;
KW secondary scent determination; polypeptide library; odour receptor;
KW scent profile; scent fingerprint; scent representation.
XX
OS Mus musculus.
XX
PN WO200127158-A2.
XX
PD 19-APR-2001.
XX
PF 06-OCT-2000; 2000WO-US27582.
XX
PR 08-OCT-1999; 99US-0158615.
PR 24-FEB-2000; 2000US-0184809.
XX
PA (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
XX
DR WPI; 2001-290713/30.
XX
PT New polynucleotides which encode polypeptides involved in olfactory
PT sensation for identifying olfactory agonists and antagonists -
XX
PS Example 6; Page 1618-1619; 1857pp; English.
XX
CC The present sequence is a polypeptide encoded by one of 105 newly mined
CC mouse genes. It was used as a query sequence in a database search of
CC olfactory receptor (OR)-like sequences. The invention relates to isolated
CC polynucleotides encoding polypeptides involved in olfactory sensation.
CC The polynucleotides can be used in screening for olfactory agonists and
CC antagonists. The methods allow for the determination of primary scents
CC and the identification of the odour receptors used to detect these
CC primary scents. The methods also enable determination of secondary scents
CC and the identification of combinations of odour receptors that are
CC involved in detecting such secondary scents. This enables the
CC construction of a scent representation (also called a scent fingerprint
CC or scent profile), which may be used to re-create and edit scents.
CC Libraries of olfactory receptors are useful for determining the
CC interaction pattern of a composition with the receptors, and can be
CC used for determining differences in the olfactory faculties of different
CC individuals.
XX
SQ Sequence 327 AA;

Query Match 85.7%; Score 1380; DB 22; Length 327;
Best Local Similarity 85.6%; Pred. No. 4e-146;
Matches 262; Conservative 20; Mismatches 24; Indels 0; Gaps 0;

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Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              | :|||||||||:|||||| |||:|||: |:  ||||| || ||::  |||| || |||
Db          3 MGALNQTRVTEFIFLGLTDNWVLEILFFVPFTVTYMLTLLGNFLIVVTIVFTPRLHNPMY 62

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
              |||||||||||||||||||||||||||||||||||||||| ||||||||||:|||||  |:||
Db         63 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCIAQLFFLHLFACSEIFLLTIMAY 122

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
              ||||||| |||| |||||:||:||||||||||:||| ||||||||||||||||||||||
Db        123 DRYVAICIPLHYSNVMNMKVCVQLVFALWLGGTIHSLVQTFLTIRLPYCGPNIIDSYFCD 182

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTC 240
              || |||||||||||||||:|||||| ||||:|||| ||| |||| |||||:||||||
Db        183 VPPVIKLACTDTYLTGILIVSNSGTISLVCFLALVTSYTVILFSLRKKSAEGRRKALSTC 242

Qy        241 SAHFMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300
              ||||||| ||||||||:||||||:|||||||||||||||||| ||||||||||:|||
Db        243 SAHFMVVTLFFGPCIFLYTRPDSSFSIDKVVSVFYTVVTPLLNPLIYTLRNEEVKTAMKH 302

Qy        301 LRQRQV 306
              ||||::
Db        303 LRQRRI 308
```

RESULT 6
AAG72706
ID AAG72706 standard; Protein; 330 AA.
XX
AC AAG72706;
XX
DT 31-JUL-2001 (first entry)
XX
DE Murine OR-like polypeptide query sequence, SEQ ID NO: 2388.
XX
KW Mouse; olfactory receptor; OR; primary scent determination;
KW secondary scent determination; polypeptide library; odour receptor;
KW scent profile; scent fingerprint; scent representation.
XX
OS Mus musculus.
XX
PN WO200127158-A2.
XX
PD 19-APR-2001.
XX
PF 06-OCT-2000; 2000WO-US27582.
XX
PR 08-OCT-1999; 99US-0158615.
PR 24-FEB-2000; 2000US-0184809.
XX
PA (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
XX
DR WPI; 2001-290713/30.
XX
PT New polynucleotides which encode polypeptides involved in olfactory
PT sensation for identifying olfactory agonists and antagonists -
XX
PS Example 6; Page 1619-1620; 1857pp; English.
XX
CC The present sequence is a polypeptide encoded by one of 105 newly mined

CC mouse genes. It was used as a query sequence in a database search of
CC olfactory receptor (OR)-like sequences. The invention relates to isolated
CC polynucleotides encoding polypeptides involved in olfactory sensation.
CC The polynucleotides can be used in screening for olfactory agonists and
CC antagonists. The methods allow for the determination of primary scents
CC and the identification of the odour receptors used to detect these
CC primary scents. The methods also enable determination of secondary scents
CC and the identification of combinations of odour receptors that are
CC involved in detecting such secondary scents. This enables the
CC construction of a scent representation (also called a scent fingerprint
CC or scent profile), which may be used to re-create and edit scents.
CC Libraries of olfactory receptors are useful for determining the
CC interaction pattern of a composition with the receptors, and can be
CC used for determining differences in the olfactory faculties of different
CC individuals.
XX
SQ Sequence 330 AA;

Query Match 61.6%; Score 992; DB 22; Length 330;
Best Local Similarity 60.6%; Pred. No. 1.4e-102;
Matches 183; Conservative 47; Mismatches 72; Indels 0; Gaps 0;

```
Qy          4 LNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMYFFL 63
              :||| |  |   ||: |  ::|  |  |   |:||| |||||::  :    |||||||||
Db          7 INQTSVMSFRLTGLSTNPKVQMAIFFIFLIFYVLTLVGNILIVVTIIHDHRLHTPMYFFL 66

Qy         64 SNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAYDRY 123
              |||||||:|||:|||||||     | | ||||:|: |:||||||| |||||| ::|||||
Db         67 SNLSFIDVCHSTVTVPKMLSDTFSEEKLISFDDCVVQIFFLHLFACTEIFLLTVMAYDRY 126

Qy        124 VAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCDVPL 183
              ||||  || |  :|| :||: |  |:|  ||:||:  | |||:||||||| :||:|||||
Db        127 VAICKPLRYMTIMNWKVCMVLGGAMWTAGTIHSISFTSLTIKLPYCGPNELDSFFCDVPQ 186

Qy        184 VIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTCSAH 243
              ||:|||||| :| ||:|:||| ||: ||: :| || |||||||:  ::|::|||||:||
Db        187 VIELACTDTRITEILVVSNSGMISMVCFVIIVVSYAVILVSLRQQISDGKRKALSTCAAH 246

Qy        244 FMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQLRQ 303
               || || | |||||:||  |   ||:|| |:| :|||||| ||| |||::|||:|:| :
Db        247 LTVVTLFLGHCIFIYSRPAISLPEDKIVSAFFTAITPLLNPIIYTFRNEDMKSALKKLIR 306

Qy        304 RQ 305
              |:
Db        307 RK 308
```

RESULT 7
AAG72080
ID AAG72080 standard; Protein; 335 AA.
XX
AC AAG72080;
XX
DT 31-JUL-2001 (first entry)
XX
DE Human olfactory receptor polypeptide, SEQ ID NO: 1761.
XX
KW Human; olfactory receptor; OR; primary scent determination;
KW secondary scent determination; polypeptide library; odour receptor;
KW scent profile; scent fingerprint; scent representation.
XX
OS Homo sapiens.
XX
PN WO200127158-A2.
XX
PD 19-APR-2001.
XX
PF 06-OCT-2000; 2000WO-US27582.
XX
PR 08-OCT-1999; 99US-0158615.
PR 24-FEB-2000; 2000US-0184809.
XX
PA (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
XX
DR WPI; 2001-290713/30.
XX
PT New polynucleotides which encode polypeptides involved in olfactory
PT sensation for identifying olfactory agonists and antagonists -
XX
PS Claim 11; Page 1155-1156; 1857pp; English.
XX
CC The present sequence is an olfactory receptor which is encoded by
CC one of a number of novel polynucleotides. The polynucleotides can be
CC used in screening for olfactory agonists and antagonists. The methods
CC allow for the determination of primary scents and the identification
CC of the odour receptors used to detect these primary scents. The methods
CC also enable determination of secondary scents and the identification of
CC combinations of odour receptors that are involved in detecting such
CC secondary scents. This enables the construction of a scent representation
CC (also called a scent fingerprint or scent profile), which may be used to
CC re-create and edit scents. Libraries of olfactory receptors are useful
CC for determining the interaction pattern of a composition with the
CC receptors, and can be used for determining differences in the olfactory
CC faculties of different individuals.
XX
SQ Sequence 335 AA;

Query Match 61.1%; Score 985; DB 22; Length 335;
Best Local Similarity 63.2%; Pred. No. 8.9e-102;
Matches 192; Conservative 38; Mismatches 72; Indels 2; Gaps 2;

```
Qy          4 LNQTR-VTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMYFF 62
              ||||  || |   ||: |   :  |  |   |:||| ||:||:|  ::   ||||||||
Db          7 LNQTSLVTYFRLRGLSVNHKARIAMFSMFLIFYVLTLIGNVLIVITIIYDHRLHTPMYFF 66

Qy         63 LSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAYDR 122
              ||||||||:|||:|||||||  :  | | |||| |:||:|||||||| ||||| ::||||
Db         67 LSNLSFIDVCHSTVTVPKMLRDVWSEEKLISFDACVTQMFFLHLFACTEIFLLTVMAYDR 126

Qy        123 YVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCDVP 182
              ||||| || |  ||| :||: |  ||| |||:||:  | |||:||||||: ||::|||||
Db        127 YVAICKPLQYMIVMNWKVCVLLAVALWTGGTIHSIALTSLTIKLPYCGPDEIDNFFCDVP 186

Qy        183 LVIKLACTDT-YLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTCS 241
              |||||| || |:  ||||:||| ||: ||: :| || |||||||:  ::|: |||||||:
Db        187 QVIKLACIDTPYVLEILIVSNSGLISVVCFVVLVVSYAVILVSLRQQISKGKWKALSTCA 246

Qy        242 AHFMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQL 301
              ||  || || | |||||:|| ||   || ||||:| ||||||| ||||||||:|||: :|
Db        247 AHLTVVTLFLGHCIFIYSRPSTSLPEDKAVSVFFTAVTPLLNPIIYTLRNEEMKSALNKL 306

Qy        302 RQRQ 305
              |:
Db        307 VGRK 310
```

RESULT 8
AAU24670
ID AAU24670 standard; Protein; 311 AA.
XX
AC AAU24670;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human olfactory receptor AOLFR168.
XX
KW Human; olfactory receptor; G protein-coupled receptor; GPCR; odourant;
KW food additive; cosmetic; fragrance; pharmaceutical additive.
XX
OS Homo sapiens.
XX
PN WO200168805-A2.
XX

```
PD   20-SEP-2001.
XX
PF   13-MAR-2001; 2001WO-US07771.
XX
PR   13-MAR-2000; 2000US-0188914.
PR   24-MAR-2000; 2000US-0192033.
PR   12-APR-2000; 2000US-0198474.
PR   24-APR-2000; 2000US-0199335.
PR   26-MAY-2000; 2000US-0207702.
PR   23-JUN-2000; 2000US-0213849.
PR   16-AUG-2000; 2000US-0226534.
PR   07-SEP-2000; 2000US-0230732.
PR   07-FEB-2001; 2001US-0266862.
XX
PA   (SENO-) SENOMYX INC.
XX
PI   Zozulya S;
XX
DR   WPI; 2001-570867/64.
DR   N-PSDB; AAS42363.
XX
PT   Nucleic acids encoding human olfactory G protein-coupled receptors,
PT   useful for screening for compounds involved in olfactory sensation,
PT   where the compounds can be used in the food, pharmaceutical and
PT   cosmetic industries to customise odours -
XX
PS   Claim 60; Page 152-153; 319pp; English.
XX
CC   The invention relates to nucleic acids encoding human olfactory
CC   receptors, OR, (a G protein-coupled receptor, GPCR). The OR's
CC   specifically recognise molecules, odourants, that elicit specific
CC   olfactory sensation. The human olfactory receptors and polynucleotides
CC   encoding them are useful for screening a library of chemical compounds
CC   for compounds that are involved in olfactory sensation. Modulators of
CC   their activity are useful for pharmacological and genetic modulation of
CC   olfactory signalling pathways. Therefore, they can be used in the food,
CC   pharmaceutical and cosmetic industries to customise odours and
CC   fragrances. The present sequence is a human olfactory receptor of the
CC   invention.
XX
SQ   Sequence   311 AA;

  Query Match             58.2%;  Score 938;  DB 22;  Length 311;
  Best Local Similarity   55.4%;  Pred. No. 1.5e-96;
  Matches  170;  Conservative   59;  Mismatches   76;  Indels    2;  Gaps    1;

Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              |: :|   ||||:| ||: :  :| : |: ||  |:: | ||:||::    :    :|||
Db          1 MEKIN--NVTEFIFWGLSQSPEIEKVCFVVFSFFYIIILLGNLLIMLTVCLSNLFKSPMY 58

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
              |||| |||:|||:|||| |||:  || : ||||:  |: ||  :| | | |||:| ::||
Db         59 FFLSFLSFVDICYSSVTAPKMIVDLLAKDKTISYVGCMLQLLGVHFFGCTEIFILTVMAY 118

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
              ||||||| |||| :||  | :::   |:|| :||: |  | ::||:|||| || ||||
Db        119 DRYVAICKPLHYMTIMNRETCNKMLLGTWVGGFLHSIIQVALVVQLPFCGPNEIDHYFCD 178

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTC 240
              |  |:|||||:||: |:::  |||||:|  |: :: || :||||||| |||||:||||||
Db        179 VHPVLKLACTETYIVGVVVTANSGTIALGSFVILLISYSIILVSLRKQSAEGRRKALSTC 238

Qy        241 SAHFMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300
              :|  :| :||||| |:| ||||:|| ||:|:||||::||:||| |||||| |||:|||:
Db        239 GSHIAMVVIFFGPCTFMYMRPDTTFSEDKMVAVFYTIITPMLNPLIYTLRNAEVKNAMKK 298

Qy        301 LRQRQVF 307
              |  | ||
Db        299 LWGRNVF 305


RESULT 9
AAG72291
ID   AAG72291 standard; Protein; 311 AA.
XX
AC   AAG72291;
XX
DT   30-JUL-2001  (first entry)
XX
DE   Human olfactory receptor polypeptide, SEQ ID NO: 1972.
XX
KW   Human; olfactory receptor; OR; primary scent determination;
KW   secondary scent determination; polypeptide library; odour receptor;
KW   scent profile; scent fingerprint; scent representation.
XX
OS   Homo sapiens.
XX
PN   WO200127158-A2.
XX
PD   19-APR-2001.
XX
PF   06-OCT-2000; 2000WO-US27582.
XX
PR   08-OCT-1999;   99US-0158615.
PR   24-FEB-2000; 2000US-0184809.
XX
PA   (DIGI-) DIGISCENTS.
PA   (YEDA ) YEDA RES & DEV CO LTD.
XX
PI   Bellenson J,  Smith D,  Lancet D,  Glusman G,  Fuchs T,  Yanai I;
XX
DR   WPI; 2001-290713/30.
XX
PT   New polynucleotides which encode polypeptides involved in olfactory
PT   sensation for identifying olfactory agonists and antagonists -
XX
PS   Claim 11; Page 1320-1321; 1857pp; English.
XX
CC   The present sequence is an olfactory receptor which is encoded by
CC   one of a number of novel polynucleotides. The polynucleotides can be
CC   used in screening for olfactory agonists and antagonists. The methods
CC   allow for the determination of primary scents and the identification
CC   of the odour receptors used to detect these primary scents. The methods
CC   also enable determination of secondary scents and the identification of
CC   combinations of odour receptors that are involved in detecting such
CC   secondary scents. This enables the construction of a scent representation
CC   (also called a scent fingerprint or scent profile), which may be used to
CC   re-create and edit scents. Libraries of olfactory receptors are useful
CC   for determining the interaction pattern of a composition with the
CC   receptors, and can be used for determining differences in the olfactory
CC   faculties of different individuals.
XX
SQ   Sequence   311 AA;

  Query Match             58.2%;  Score 938;  DB 22;  Length 311;
  Best Local Similarity   55.4%;  Pred. No. 1.5e-96;
  Matches  170;  Conservative   59;  Mismatches   76;  Indels    2;  Gaps    1;

Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              |: :|   ||||:| ||: :  :| : |: ||  |:: | ||:||::    :    :|||
Db          1 MEKIN--NVTEFIFWGLSQSPEIEKVCFVVFSFFYIIILLGNLLIMLTVCLSNLFKSPMY 58

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
              |||| |||:|||:|||| |||:  || : ||||:  |: ||  :| | | |||:| ::||
Db         59 FFLSFLSFVDICYSSVTAPKMIVDLLAKDKTISYVGCMLQLLGVHFFGCTEIFILTVMAY 118

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
              ||||||| |||| :||  | :::   |:|| :||: |  | ::||:|||| || ||||
Db        119 DRYVAICKPLHYMTIMNRETCNKMLLGTWVGGFLHSIIQVALVVQLPFCGPNEIDHYFCD 178

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTC 240
              |  |:|||||:||: |:::  |||||:|  |: :: || :||||||| |||||:||||||
Db        179 VHPVLKLACTETYIVGVVVTANSGTIALGSFVILLISYSIILVSLRKQSAEGRRKALSTC 238

Qy        241 SAHFMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300
              :|  :| :||||| |:| ||||:|| ||:|:||||::||:||| |||||| |||:|||:
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```
Db        239 GSHIAMVVIFFGPCTFMYMRPDTTFSEDKMVAVFYTIITPMLNPLIYTLRNAEVKNAMKK 298

Qy        301 LRQRQVF 307
              | | ||
Db        299 LWGRNVF 305


RESULT 10
ABP95716
ID   ABP95716 standard; Protein; 311 AA.
XX
AC   ABP95716;
XX
DT   06-MAR-2003  (first entry)
XX
DE   Human GPCR polypeptide SEQ ID NO 242.
XX
KW   Human; GPCR; G protein coupled receptor; signal transduction; olfactory;
KW   drug development; gustatory; taste; fragrance; receptor.
XX
OS   Homo sapiens.
XX
PN   WO200216548-A2.
XX
PD   28-FEB-2002.
XX
PF   30-JUL-2001; 2001WO-IB01446.
XX
PR   04-AUG-2000; 2000JP-0237818.
PR   13-FEB-2001; 2001JP-0034434.
XX
PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI   Haga T,  Takeda S,  Mitaku S;
XX
DR   WPI; 2002-304118/34.
DR   N-PSDB; ABZ42990.
XX
PT   Database global search for G protein-coupled receptors, proteins and
PT   encoded genes for studying in vivo signal transduction mechanism and
PT   identifying targets for drug development  -
XX
PS   Claim 10; SEQ ID NO 242; 97pp + Sequence Listing; Japanese.
XX
CC   The invention relates to a method for screening G protein-coupled
CC   receptor (GPCR) genes (ABZ42870-ABZ43216) and/or GPCR proteins
CC   (ABP95596-ABP95942) by extracting open-reading frames containing 6-8
CC   transmembrane domains with 250-1000 amino acid residues to give a gene
CC   homologous with a known GPCR gene. The receptor proteins and encoded
CC   genes are useful for studying in vivo signal transduction mechanism and
CC   identifying targets for drug development e.g. based on olfactory and
CC   gustatory receptors in form of agonists and antagonists by screening
CC   intrinsic and extrinsic ligands as bitter taste inhibitors, taste
CC   enhancers and fragrance improvers.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   311 AA;

  Query Match             58.2%;  Score 938;  DB 23;  Length 311;
  Best Local Similarity   55.4%;  Pred. No. 1.5e-96;
  Matches  170;  Conservative   59;  Mismatches   76;  Indels    2;  Gaps    1;

Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              |: :|   ||||:| ||: :  :| : |: ||  |:: | ||:||::    :    :|||
Db          1 MEKIN--NVTEFIFWGLSQSPEIEKVCFVVFSFFYIIILLGNLLIMLTVCLSNLFKSPMY 58

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
              |||| |||:|||:|||| |||:  || : ||||:  |: ||  :| | | |||:| ::||
Db         59 FFLSFLSFVDICYSSVTAPKMIVDLLAKDKTISYVGCMLQLLGVHFFGCTEIFILTVMAY 118

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
              ||||||| |||| :||  | :::  |:|| :||: |  | ::||:|||| || ||||
Db        119 DRYVAICKPLHYMTIMNRETCNKMLLGTWVGGFLHSIIQVALVVQLPFCGPNEIDHYFCD 178

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTC 240
              |  |:|||||:||: |::  |||||:|  |: :: || :||||||| |||||:||||||
Db        179 VHPVLKLACTETYIVGVVVTANSGTIALGSFVILLISYSIILVSLRKQSAEGRRKALSTC 238

Qy        241 SAHFMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300
              :|  :| :||||| |:| ||||:|| ||:|:|||||::||:||| |||||| |||:|||:
Db        239 GSHIAMVVIFFGPCTFMYMRPDTTFSEDKMVAVFYTIITPMLNPLIYTLRNAEVKNAMKK 298

Qy        301 LRQRQVF 307
              | | ||
Db        299 LWGRNVF 305


RESULT 11
AAB71364
ID   AAB71364 standard; Protein; 311 AA.
XX
AC   AAB71364;
XX
DT   19-NOV-2002  (first entry)
XX
DE   Human GCREC-43 INCYTE ID 7475214CD1 SEQ ID 43.
XX
KW   GCREC; Human; G-protein coupled receptor; anti-HIV; antiarteriosclerotic;
KW   cytostatic; neuroprotective; antiparkinsonian; hepatotropic; laxative;
KW   cerebroprotective; antiinflammatory; virucide; antibacterial; fungicide;
KW   protozoacide; cirrhosis; cancer; stroke; Alzheimer's disease; AIDS;
KW   Parkinson's disease; Crohn's disease; constipation; infection; receptor;
KW   gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO200263004-A2.
XX
PD   15-AUG-2002.
XX
PF   06-FEB-2002; 2002WO-US03635.
XX
PR   07-FEB-2001; 2001US-267322P.
PR   23-FEB-2001; 2001US-271215P.
PR   08-MAR-2001; 2001US-274551P.
PR   23-MAR-2001; 2001US-278507P.
PR   30-MAR-2001; 2001US-280597P.
PR   02-APR-2001; 2001US-281107P.
PR   06-APR-2001; 2001US-282121P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Baughn MR,  Tribouley CM,  Nguyen DB,  Thornton M,  Yao MG;
PI   Kallick DA,  Gandhi AR,  Walia NK,  Arvizu C,  Elliott VS;
PI   Hafalia AJA,  Ramkumar J,  Pei J,  Tang YT,  Yue H,  Reddy R;
PI   Butford N,  Lu DAM,  Graul RC,  Khan FA,  Walsh RT,  Ison CH;
PI   Richardson TW,  Griffin JA,  Warren BA,  Yang J,  Lee EA,  Harland L;
XX
DR   WPI; 2002-627557/67.
DR   N-PSDB; AAF88622.
XX
PT   New human G-protein coupled receptors (GCREC), useful for diagnosing or
PT   treating a disease or condition associated with decreased expression or
PT   over expression of functional GCRECs e.g. cancer, Alzheimer's and
PT   Parkinson's -
XX
PS   Claim 104; Page 204; 239pp; English.
XX
CC   This invention describes novel polypeptides which have anti-HIV,
CC   antiarteriosclerotic, cytostatic, neuroprotective, antiparkinsonian,
CC   hepatotropic, laxative, cerebroprotective, antiinflammatory, virucide,
CC   antibacterial, fungicide and protozoacide activity. The products of the
CC   invention are useful for treating a disease or condition associated with
CC   decreased expression or over expression of functional G-protein coupled
```

```
CC   receptors (GCREC), while antibodies generated against the polypeptide of
CC   the invention are useful for diagnosing a condition or disease associated
CC   with the expression of GCREC e.g. arteriosclerosis, cirrhosis, cancer,
CC   stroke, Alzheimer's disease, Parkinson's disease, Crohn's disease,
CC   constipation, AIDS, or bacterial, viral, fungal or protozoal infections.
CC   The compounds described in the invention can be used for gene therapy.
CC   AAB71322-AAB71369 represent the GCREC proteins encoded by
CC   AAF88580-AAF88627 described in the disclosure of the invention.
XX
SQ   Sequence   311 AA;

  Query Match             58.2%;  Score 938;  DB 23;  Length 311;
  Best Local Similarity   55.4%;  Pred. No. 1.5e-96;
  Matches  170;  Conservative   59;  Mismatches   76;  Indels    2;  Gaps    1;

Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              |: :|   ||||:| ||: :  :| : |: ||  |:: | ||:||::    :    :|||
Db          1 MEKIN--NVTEFIFWGLSQSPEIEKVCFVVFSFFYIIILLGNLLIMLTVCLSNLFKSPMY 58

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
              |||| |||:|||:|||| |||:  || : ||||:  |: ||  :| | | |||:| ::||
Db         59 FFLSFLSFVDICYSSVTAPKMIVDLLAKDKTISYVGCMLQLLGVHFFGCTEIFILTVMAY 118

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
              ||||||| |||| :||   | :::   |:|| :||: |  | ::||:|||| || ||||
Db        119 DRYVAICKPLHYMTIMNRETCNKMLLGTWVGGFLHSIIQVALVVQLPFCGPNEIDHYFCD 178

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTC 240
              |  |:|||||:||: |:::  |||||:|  |: :: || :|||||.| |||||:|||||||
Db        179 VHPVLKLACTETYIVGVVVTANSGTIALGSFVILLISYSIILVSLRKQSAEGRRKALSTC 238

Qy        241 SAHFMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300
               :|  :| :||||| |:| ||||:|| ||:|:||||::||:||| |||||| |||:|||:
Db        239 GSHIAMVVIFFGPCTFMYMRPDTTFSEDKMVAVFYTIITPMLNPLIYTLRNAEVKNAMKK 298

Qy        301 LRQRQVF 307
              | | ||
Db        299 LWGRNVF 305


RESULT 12
AAU95650
ID   AAU95650 standard; Protein; 311 AA.
XX
AC   AAU95650;
XX
DT   02-JUL-2002  (first entry)
XX
DE   Human olfactory and pheromone G protein-coupled receptor #137.
XX
KW   Human; olfactory and pheromone G protein coupled; receptor;
KW   GPCR; tranquilizer; antidepressant; neuroleptic; endocrine; anabolic;
KW   anorectic; taste; fragrance; food additive; cosmetic; cell migration;
KW   sterility; psychotic disorder; neurological disorder; anxiety;
KW   schizophrenia; manic depression; depression; axonal growth;
KW   menstrual cycle; appetite sexual motivation; sexual attraction;
KW   aggression.
XX
OS   Homo sapiens.
XX
PN   WO200224726-A2.
XX
PD   28-MAR-2002.
XX
PF   21-SEP-2001; 2001WO-BE00162.
XX
PR   22-SEP-2000; 2000EP-0870211.
XX
PA   (CHEM-) CHEMCOM SA.
XX
PI   Veithen A;
XX
DR   WPI; 2002-330013/36.
DR   N-PSDB; ABK68537.
XX
PT   Novel pheromone G-protein coupled receptor and receptor-derived
PT   agonists, antagonists or inhibitors useful in food or cosmetic products
PT   or in the treatment or prevention of neurological disorders such as
PT   anxiety and schizophrenia -
XX
PS   Disclosure; Page 423-424; 833pp; English.
XX
CC   The invention relates to olfactory and Pheromone G-protein coupled
CC   receptor (GPCR) or a protein 95% identical to the GPCR, a specific active
CC   portion and its encoding polynucleotide. Also included are an agonist,
CC   antagonist or inhibitor of the GPCR or the polynucleotide, a vector
CC   comprising the polynucleotide, a cell transformed by the vector, a non-
CC   human mammal comprising a partial or total deletion of the polynucleotide
CC   encoding the receptor and screening (detection and possibly, recovering)
CC   of compounds which are known or not known to be agonist, antagonists or
CC   inhibitors of natural compounds to the GPCR. The receptor-derived
CC   agonists, antagonists, inhibitors or compounds are used as an
CC   improvement, elimination or substitution of an existing taste and/or a
CC   fragrance of (or in) the food and/or cosmetic products. They can also be
CC   used in the preparation of medicament in the treatment and/or prevention
CC   of a mammalian disorder, such as cell migration, sterility, psychotic and
CC   neurological disorders, including anxiety, schizophrenia, manic
CC   depression, depression, for promoting axonal growth, nerve cell
CC   connection and nerve regeneration for modulating male and female
CC   endocrine functions, hormone production and the menstrual cycle, for the
CC   prevention or the treatment by stimulation of several mammalian
CC   behaviours, such as stimulation or suppression of appetite, sexual
CC   motivation, sexual attraction, aggression and for promoting or
CC   suppressing chemical communication between organisms. The present
CC   sequence is a human olfactory and pheromone GPCR protein sequence.
XX
SQ   Sequence   311 AA;

  Query Match             58.2%;  Score 938;  DB 23;  Length 311;
  Best Local Similarity   55.4%;  Pred. No. 1.5e-96;
  Matches  170;  Conservative   59;  Mismatches   76;  Indels    2;  Gaps    1;

Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              |: :|   ||||:| ||: :  :| : |: ||  |:: | ||:||::    :    :|||
Db          1 MEKIN--NVTEFIFWGLSQSPEIEKVCFVVFSFFYIIILLGNLLIMLTVCLSNLFKSPMY 58

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
              |||| |||:|||:|||| |||:  || : ||||:  |: ||  :| | | |||:| ::||
Db         59 FFLSFLSFVDICYSSVTAPKMIVDLLAKDKTISYVGCMLQLLGVHFFGCTEIFILTVMAY 118

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
              ||||||| |||| :||   | :::   |:|| :||: |  | ::||:|||| || ||||
Db        119 DRYVAICKPLHYMTIMNRETCNKMLLGTWVGGFLHSIIQVALVVQLPFCGPNEIDHYFCD 178

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTC 240
              |  |:|||||:||: |:::  |||||:|  |: :: || :|||||.| |||||:|||||||
Db        179 VHPVLKLACTETYIVGVVVTANSGTIALGSFVILLISYSIILVSLRKQSAEGRRKALSTC 238

Qy        241 SAHFMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300
               :|  :| :||||| |:| ||||:|| ||:|:||||::||:||| |||||| |||:|||:
Db        239 GSHIAMVVIFFGPCTFMYMRPDTTFSEDKMVAVFYTIITPMLNPLIYTLRNAEVKNAMKK 298

Qy        301 LRQRQVF 307
              | | ||
Db        299 LWGRNVF 305


RESULT 13
AAU85290
ID   AAU85290 standard; Protein; 311 AA.
XX
AC   AAU85290;
XX
DT   08-MAY-2002  (first entry)
XX
DE   G-coupled olfactory receptor #151.
```

```
XX
KW   Human; olfactory G-coupled receptor; sensory perception of odourant;
KW   odour composition; taste composition.
XX
OS   Homo sapiens.
XX
PN   WO200198526-A2.
XX
PD   27-DEC-2001.
XX
PF   22-JUN-2001; 2001WO-US20122.
XX
PR   22-JUN-2000; 2000US-213812P.
PR   13-MAR-2001; 2001US-0804291.
XX
PA   (SENO-) SENOMYX INC.
XX
PI   Zozulya S,  Stryer L;
XX
DR   WPI; 2002-083330/11.
DR   N-PSDB; ABK37649.
XX
PT   Representing sensory perception of one or more odourants for the
PT   identification and design of tastes and odours comprises providing a
PT   representative group of n olfactory receptors -
XX
PS   Claim 1; Page 126; 182pp; English.
XX
CC   The invention relates to a method of representing sensory perception of
CC   one or more odourants. The method comprises: (a) providing a
CC   representative class of n olfactory receptors or ligand binding domains
CC   (LBD) of these receptors; (b) measuring values X1 to Xn representative
CC   of at least one activity of one or more odourants selected from:
CC   (i) binding one or more odourants to the LBD of at least one of the n
CC   olfactory receptors; (ii) activating at least one of the n
CC   olfactory receptors with the one or more odourants; and (iii) blocking at
CC   least one of the n olfactory receptors with the one or more odourants;
CC   and (c) generating a representation of sensory perception from the values
CC   X1 to Xn. The representation of the sensory perception of odourants is
CC   useful for the design and formulation of odour and taste compositions.
CC   AAU85140-AAU85393 represent human olfactory G-coupled receptor amino acid
CC   sequences of the invention.
XX
SQ   Sequence   311 AA;

  Query Match             58.2%;  Score 938;  DB 23;  Length 311;
  Best Local Similarity   55.4%;  Pred. No. 1.5e-96;
  Matches  170;  Conservative   59;  Mismatches   76;  Indels    2;  Gaps    1;

Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              |: :|   ||||:| ||: :  :| : |: ||  |:: | ||:||::    :    :|||
Db          1 MEKIN--NVTEFIFWGLSQSPEIEKVCFVVFSFFYIIILLGNLLIMLTVCLSNLFKSPMY 58

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
              |||| |||:|||:|||| |||:  || : ||||:  |: ||  :| || | |||:| ::||
Db         59 FFLSFLSFVDICYSSVTAPKMIVDLLAKDKTISYVGCMLQLLGVHFFGCTEIFILTVMAY 118

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
              ||||||| ||||  :||   | :::   |:|| :||: |  | ::||:|||| || ||||
Db        119 DRYVAICKPLHYMTIMNRETCNKMLLGTWVGGFLHSIIQVALVVQLPFCGPNEIDHYFCD 178

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTC 240
              |  |:|||||:||: |:::  |||||:|  |: :: || :|||||| |||||:||||||
Db        179 VHPVLKLACTETYIVGVVVTANSGTIALGSFVILLISYSIILVSLRKQSAEGRRKALSTC 238

Qy        241 SAHFMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300
              :|  :| :|||| |:| |||:|| ||:|:||||::||:||| |||||| |||:|||:
Db        239 GSHIAMVVIFFGPCTFMYMRPDTTFSEDKMVAVFYTIITPMLNPLIYTLRNAEVKNAMKK 298

Qy        301 LRQRQVF 307
              | | ||
Db        299 LWGRNVF 305
```

```
RESULT 14
AAG71471
ID   AAG71471 standard; Protein; 314 AA.
XX
AC   AAG71471;
XX
DT   30-JUL-2001  (first entry)
XX
DE   Human olfactory receptor polypeptide, SEQ ID NO: 1152.
XX
KW   Human; olfactory receptor; OR; primary scent determination;
KW   secondary scent determination; polypeptide library; odour receptor;
KW   scent profile; scent fingerprint; scent representation.
XX
OS   Homo sapiens.
XX
PN   WO200127158-A2.
XX
PD   19-APR-2001.
XX
PF   06-OCT-2000; 2000WO-US27582.
XX
PR   08-OCT-1999;   99US-0158615.
PR   24-FEB-2000; 2000US-0184809.
XX
PA   (DIGI-) DIGISCENTS.
PA   (YEDA ) YEDA RES & DEV CO LTD.
XX
PI   Bellenson J,  Smith D,  Lancet D,  Glusman G,  Fuchs T,  Yanai I;
XX
DR   WPI; 2001-290713/30.
XX
PT   New polynucleotides which encode polypeptides involved in olfactory
PT   sensation for identifying olfactory agonists and antagonists -
XX
PS   Claim 11; Page 671-672; 1857pp; English.
XX
CC   The present sequence is an olfactory receptor which is encoded by
CC   one of a number of novel polynucleotides. The polynucleotides can be
CC   used in screening for olfactory agonists and antagonists. The methods
CC   allow for the determination of primary scents and the identification
CC   of the odour receptors used to detect these primary scents. The methods
CC   also enable determination of secondary scents and the identification of
CC   combinations of odour receptors that are involved in detecting such
CC   secondary scents. This enables the construction of a scent representation
CC   (also called a scent fingerprint or scent profile), which may be used to
CC   re-create and edit scents. Libraries of olfactory receptors are useful
CC   for determining the interaction pattern of a composition with the
CC   receptors, and can be used for determining differences in the olfactory
CC   faculties of different individuals.
XX
SQ   Sequence   314 AA;

  Query Match             57.7%;  Score 929;  DB 22;  Length 314;
  Best Local Similarity   53.1%;  Pred. No. 1.6e-95;
  Matches  165;  Conservative   67;  Mismatches   79;  Indels    0;  Gaps    0;

Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              ||  |:: ::||| |||:::  |:| ||| || :|: |: || ||:|  :  | ||:|||
Db          1 MDVGNKSTMSEFVLLGLSNSWELQMFFFMVFSLLYVATMVGNSLIVITVIVDPHLHSPMY 60

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
              | |:||| ||:  :|   |||:   |   |||||| |:||:|||||   || ||: :::
Db         61 FLLTNLSIIDMSLASFATPKMITDYLTGHKTISFDGCLTQIFFLHLFTGTEIILLMAMSF 120

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
              |||:||| |||| :|:: :||: || | |: | :||: |    : ||:|||  :||:|||
Db        121 DRYIAICKPLHYASVISPQVCVALVVASWIMGVMHSMSQVIFALTLPFCGPYEVDSFFCD 180

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTC 240
              :|:| :||| |||: |: ::: || |:|||: :  ||:::|:::  ||: |  ||||||
Db        181 LPVVFQLACVDTYVLGLFMISTSGIIALSCFIVLFNSYVIVLVTVKHHSSRGSSKALSTC 240
```

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Qy        241 SAHFMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300
              :|||:|| |||||||||| | :|| ||::|||||: || ||| ||||||:||| ||::
Db        241 TAHFIVVFLFFGPCIFIYMWPLSSFLTDKILSVFYTIFTPTLNPIIYTLRNQEVKIAMRK 300

Qy        301 LRQRQVFFTKS 311
              |: | : | |:
Db        301 LKNRFLNFNKA 311


RESULT 15
ABP95834
ID   ABP95834 standard; Protein; 314 AA.
XX
AC   ABP95834;
XX
DT   06-MAR-2003  (first entry)
XX
DE   Human GPCR polypeptide SEQ ID NO 478.
XX
KW   Human; GPCR; G protein coupled receptor; signal transduction; olfactory;
KW   drug development; gustatory; taste; fragrance; receptor.
XX
OS   Homo sapiens.
XX
PN   WO200216548-A2.
XX
PD   28-FEB-2002.
XX
PF   30-JUL-2001; 2001WO-IB01446.
XX
PR   04-AUG-2000; 2000JP-0237818.
PR   13-FEB-2001; 2001JP-0034434.
XX
PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI   Haga T,  Takeda S,  Mitaku S;
XX
DR   WPI; 2002-304118/34.
DR   N-PSDB; ABZ43108.
XX
PT   Database global search for G protein-coupled receptors, proteins and
PT   encoded genes for studying in vivo signal transduction mechanism and
PT   identifying targets for drug development  -
XX
PS   Claim 10; SEQ ID NO 478; 97pp + Sequence Listing; Japanese.
XX
CC   The invention relates to a method for screening G protein-coupled
CC   receptor (GPCR) genes (ABZ42870-ABZ43216) and/or GPCR proteins
CC   (ABP95596-ABP95942) by extracting open-reading frames containing 6-8
CC   transmembrane domains with 250-1000 amino acid residues to give a gene
CC   homologous with a known GPCR gene. The receptor proteins and encoded
CC   genes are useful for studying in vivo signal transduction mechanism and
CC   identifying targets for drug development e.g. based on olfactory and
CC   gustatory receptors in form of agonists and antagonists by screening
CC   intrinsic and extrinsic ligands as bitter taste inhibitors, taste
CC   enhancers and fragrance improvers.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   314 AA;

  Query Match             57.7%;  Score 929;  DB 23;  Length 314;
  Best Local Similarity   53.1%;  Pred. No. 1.6e-95;
  Matches  165;  Conservative   67;  Mismatches   79;  Indels    0;  Gaps    0;

Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              ||  |:: ::||| |||::  |:| ||| || :|: |: || ||:|  :  | ||:|||
Db          1 MDVGNKSTMSEFVLLGLSNSWELQMFFFMVFSLLYVATMVGNSLIVITVIVDPHLHSPMY 60

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
              | |:||| ||:  :|   |||:   |   |||||| |:||:||||||   || ||: :::

Db         61 FLLTNLSIIDMSLASFATPKMITDYLTGHKTISFDGCLTQIFFLHLFTGTEIILLMAMSF 120

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
              |||:||| |||| :|:: :||: || | |: | :||: |    : ||:|||  :||:|||
Db        121 DRYIAICKPLHYASVISPQVCVALVVASWIMGVMHSMSQVIFALTLPFCGPYEVDSFFCD 180

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTC 240
              :|:| :||| |||: |: ::: || |:|||: :  ||:::||::: ||: |  ||||||
Db        181 LPVVFQLACVDTYVLGLFMISTSGIIALSCFIVLFNSYVIVLVTVKHHSSRGSSKALSTC 240

Qy        241 SAHFMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300
              :|||:|| |||||||||| | :|| ||::|||||: || ||| ||||||:||| ||::
Db        241 TAHFIVVFLFFGPCIFIYMWPLSSFLTDKILSVFYTIFTPTLNPIIYTLRNQEVKIAMRK 300

Qy        301 LRQRQVFFTKS 311
              |: | : | |:
Db        301 LKNRFLNFNKA 311


Search completed: August 12, 2003, 16:06:45
Job time : 85 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 12, 2003, 16:01:06 ; Search time 98 Seconds
(without alignments)
824.188 Million cell updates/sec

Title: US-09-807-132-4
Perfect score: 1611
Sequence: 1 MDSLNQTRVTEFVFLGLTDN.....VKSAMKQLRQRQVFFTKSYT 313

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1611	100.0	313	4	Q8NGC2	Q8ngc2 homo sapien
2	1380	85.7	308	11	Q9R0K3	Q9r0k3 mus musculu
3	1112	69.0	213	4	Q96R62	Q96r62 homo sapien
4	1016	63.1	310	11	Q9R0K4	Q9r0k4 mus musculu
5	992	61.6	313	11	Q9R0K5	Q9r0k5 mus musculu
6	938	58.2	311	4	Q8NH73	Q8nh73 homo sapien
7	931	57.8	318	11	Q8VF96	Q8vf96 mus musculu
8	929	57.7	314	4	Q8NGD2	Q8ngd2 homo sapien
9	927.5	57.6	310	4	Q8NGD5	Q8ngd5 homo sapien
10	921	57.2	308	11	Q8VGN8	Q8vgn8 mus musculu
11	920	57.1	326	11	Q8VF11	Q8vf11 mus musculu
12	919	57.0	324	4	Q8NH41	Q8nh41 homo sapien
13	918	57.0	309	11	Q8VEZ3	Q8vez3 mus musculu
14	914	56.7	321	11	Q8VEX0	Q8vex0 mus musculu
15	912	56.6	324	11	Q8VEX3	Q8vex3 mus musculu
16	911	56.5	309	11	Q8VEZ2	Q8vez2 mus musculu
17	909	56.4	309	11	Q8VGN7	Q8vgn7 mus musculu
18	906	56.2	318	4	Q8NG74	Q8ng74 homo sapien
19	904	56.1	309	11	Q8VEY5	Q8vey5 mus musculu
20	902	56.0	304	11	Q8VGP3	Q8vgp3 mus musculu
21	900	55.9	318	4	Q8NGN0	Q8ngn0 homo sapien
22	897.5	55.7	321	11	Q8VEX1	Q8vex1 mus musculu
23	897	55.7	309	11	Q8K500	Q8k500 mus musculu
24	894.5	55.5	307	11	Q8VGN3	Q8vgn3 mus musculu
25	893	55.4	302	11	Q9R0K1	Q9r0k1 mus musculu
26	893	55.4	311	4	Q8NGD4	Q8ngd4 homo sapien
27	891	55.3	305	11	Q8VGP2	Q8vgp2 mus musculu
28	889.5	55.2	318	11	Q8VFC7	Q8vfc7 mus musculu
29	889	55.2	308	4	Q8IXE1	Q8ixe1 homo sapien
30	888.5	55.2	303	11	Q8VFF9	Q8vff9 mus musculu
31	888	55.1	311	4	Q8NGD6	Q8ngd6 homo sapien
32	883	54.8	303	11	Q8VFF8	Q8vff8 mus musculu
33	883	54.8	307	11	Q8VGF4	Q8vgf4 mus musculu
34	882	54.7	323	11	Q8VET4	Q8vet4 mus musculu
35	880.5	54.7	313	4	Q8NH05	Q8nh05 homo sapien
36	878	54.5	315	4	Q8NGC6	Q8ngc6 homo sapien
37	877	54.4	308	11	Q8VFT3	Q8vft3 mus musculu
38	877	54.4	311	11	Q8VFU9	Q8vfu9 mus musculu
39	877	54.4	314	11	Q8VFN1	Q8vfn1 mus musculu
40	874	54.3	303	11	Q8VF41	Q8vf41 mus musculu
41	873	54.2	310	11	Q8VF97	Q8vf97 mus musculu
42	873	54.2	314	4	Q8NGE8	Q8nge8 homo sapien
43	872	54.1	311	11	Q8VG74	Q8vg74 mus musculu
44	871	54.1	234	11	Q9R0G2	Q9r0g2 marmota mar
45	869	53.9	308	11	Q9R0K2	Q9r0k2 mus musculu

ALIGNMENTS

RESULT 1
Q8NGC2
ID Q8NGC2 PRELIMINARY; PRT; 313 AA.
AC Q8NGC2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Seven transmembrane helix receptor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RT "Genome-wide discovery and analysis of human seven transmembrane helix
RT receptor genes.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB065895; BAC06111.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR000985; Lectin_legA.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
DR PROSITE; PS00308; LECTIN_LEGUME_ALPHA; 1.
KW Receptor; Transmembrane.
SQ SEQUENCE 313 AA; 35466 MW; 59A922BBA6978452 CRC64;

Query Match 100.0%; Score 1611; DB 4; Length 313;
Best Local Similarity 100.0%; Pred. No. 3.2e-137;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTC 240

Qy        241 SAHFMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SAHFMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300

Qy        301 LRQRQVFFTKSYT 313
              |||||||||||||
Db        301 LRQRQVFFTKSYT 313
```

RESULT 2
Q9R0K3
ID Q9R0K3 PRELIMINARY; PRT; 308 AA.
AC Q9R0K3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Odorant receptor MOR83 (Olfactory receptor MOR244-3).
GN MOR83.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129-SvJ;
RA Tsuboi A., Yoshihara S., Yamazaki N., Kasai H., Asai-Tsuboi H.,
RA Komatsu M., Serizawa S., Ishii T., Matsuda Y., Nagawa F., Sakano H.;
RT "Olfactory neurons expressing closely linked and homologous odorant
RT receptor genes tend to project their axons to neighboring glomeruli on
RT the olfactory bulb.";
RL J. Neurosci. 0:0-0(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Zhang X., Firestein S.J.;
RT "The olfactory receptor gene superfamily of the mouse.";
RL Nat. Neurosci. 0:0-0(2002).
RN [3]
RP SEQUENCE FROM N.A.
RA Adams M.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB030894; BAA86125.1; -.
DR EMBL; AY073295; AAL60958.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 308 AA; 35015 MW; 73CFB2D1630540C5 CRC64;

Query Match 85.7%; Score 1380; DB 11; Length 308;
Best Local Similarity 85.6%; Pred. No. 2.1e-116;
Matches 262; Conservative 20; Mismatches 24; Indels 0; Gaps 0;

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Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              | :|||||||||:|||||| |||:|||: |:  ||||| || ||::  |||| || |||
Db          1 MGALNQTRVTEFIFLGLTDNWVLEILFFVPFTVTYMLTLLGNFLIVVTIVFTPRLHNPMY 60

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
              |||||||||||||||||||||||||||||||||||| ||||||||:||||| |:||
Db         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCIAQLFFLHLFACSEIFLLTIMAY 120

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
              ||||||| |||| |||||:||:|||||||||||:||| |||||||||||||||||||||||
Db        121 DRYVAICIPLHYSNVMNMKVCVQLVFALWLGGTIHSLVQTFLTIRLPYCGPNIIDSYFCD 180

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTC 240
              || |||||||||||||||:||||||| ||||:|||| ||| |||| |||||:||||||
Db        181 VPPVIKLACTDTYLTGILIVSNSGTISLVCFLALVTSYTVILFSLRKKSAEGRRKALSTC 240

Qy        241 SAHFMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300
              ||||||| |||||||:|||||:||||||||||||||||||| ||||||||||:|||
Db        241 SAHFMVVTLFFGPCIFLYTRPDSSFSIDKVVSVFYTVVTPLLNPLIYTLRNEEVKTAMKH 300

Qy        301 LRQRQV 306
              ||||::
Db        301 LRQRRI 306
```

RESULT 3
Q96R62
ID Q96R62 PRELIMINARY; PRT; 213 AA.
AC Q96R62;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Olfactory receptor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Fuchs T., Malecova B., Linhart C., Sharan R., Khen M., Herwig R.,
RA Shmulevich D., Elkon R., Steinfath M., O'Brien J.K., Radelof U.,
RA Lehrach H., Olender Z., Gluesman G., Lancet D., Shamir R.;
RT "DEFOG: A Practical Scheme for Deciphering Families of Genes.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF399581; AAK95066.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 213 213
SQ SEQUENCE 213 AA; 23792 MW; 74819DA82D5230DB CRC64;

Query Match 69.0%; Score 1112; DB 4; Length 213;
Best Local Similarity 100.0%; Pred. No. 2e-92;
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         68 FIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAYDRYVAIC 127
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 FIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAYDRYVAIC 60

Qy        128 TPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCDVPLVIKL 187
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCDVPLVIKL 120

Qy        188 ACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTCSAHFMVV 247
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTCSAHFMVV 180

Qy        248 ALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTP 280
              |||||||||||||||||||||||||||||||||
Db        181 ALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTP 213
```

RESULT 4
Q9R0K4
ID Q9R0K4 PRELIMINARY; PRT; 310 AA.
AC Q9R0K4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

```
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Odorant receptor MOR10 (Olfactory receptor MOR244-2).
GN   MOR10.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RA   Tsuboi A., Yoshihara S., Yamazaki N., Kasai H., Asai-Tsuboi H.,
RA   Komatsu M., Serizawa S., Ishii T., Matsuda Y., Nagawa F., Sakano H.;
RT   "Olfactory neurons expressing closely linked and homologous odorant
RT   receptor genes tend to project their axons to neighboring glomeruli on
RT   the olfactory bulb.";
RL   J. Neurosci. 0:0-0(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Zhang X., Firestein S.J.;
RT   "The olfactory receptor gene superfamily of the mouse.";
RL   Nat. Neurosci. 0:0-0(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Adams M.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB030893; BAA86124.1; -.
DR   EMBL; AY073294; AAL60957.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   310 AA;  34979 MW;  BAD597BB82AFEB39 CRC64;

  Query Match             63.1%;  Score 1016;  DB 11;  Length 310;
  Best Local Similarity   62.6%;  Pred. No. 1.3e-83;
  Matches  189;  Conservative   45;  Mismatches   68;  Indels    0;  Gaps    0;

Qy          4 LNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMYFFL 63
              :|:|  |   |    ||: | :::|   |   |    |:||| |||||:|  :|    |||||||||
Db          7 INETSVMSFRLTGLSTNPLVQMAVFFIFLIFYVLTLVGNILIVITIIYDRRLHTPMYFFL 66

Qy         64 SNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAYDRY 123
              |||||||:|||:|||||||      | | |||| |: |:|||||||| |||||  ::|||||
Db         67 SNLSFIDVCHSTVTVPKMLSDTFSEEKLISFDACVVQMFFLHLFACTEIFLLTVMAYDRY 126

Qy        124 VAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCDVPL 183
              |||| || |  :|| :||: |  ||| |||:||:  | |||:|||||: ||::|||||.
Db        127 VAICKPLQYMTIMNWKVCMMLAAALWTGGTIHSISLTSLTIKLPYCGPDEIDNFFCDVPQ 186

Qy        184 VIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTCSAH 243
              |||||||||::  ||||:||| ||: ||: : || |||||||:  ::|::|||||:||
Db        187 VIKLACTDTHIIEILIVSNSGLISVVCFVVLVVSYAVILVSLRQQISDGKRKALSTCAAH 246

Qy        244 FMVVALPFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQLRQ 303
                || || | |||||:|| ||   |||||||:| ||||||| |||||||::|||: :| :
Db        247 LTVVTLFLGHCIFIYSRPSTSLPEDKVVSVFFTAVTPLLNPIIYTLRNEDMKSALNKLIK 306

Qy        304 RQ 305
              |:
Db        307 RR 308


RESULT 5
Q9R0K5
ID   Q9R0K5      PRELIMINARY;      PRT;   313 AA.
AC   Q9R0K5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Odorant receptor MOR28 (Olfactory receptor MOR244-1).
GN   MOR28.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RA   Tsuboi A., Yoshihara S., Yamazaki N., Kasai H., Asai-Tsuboi H.,
RA   Komatsu M., Serizawa S., Ishii T., Matsuda Y., Nagawa F., Sakano H.;
RT   "Olfactory neurons expressing closely linked and homologous odorant
RT   receptor genes tend to project their axons to neighboring glomeruli on
RT   the olfactory bulb.";
RL   J. Neurosci. 0:0-0(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Zhang X., Firestein S.J.;
RT   "The olfactory receptor gene superfamily of the mouse.";
RL   Nat. Neurosci. 0:0-0(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Adams M.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB030892; BAA86123.1; -.
DR   EMBL; AY073251; AAL60914.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   313 AA;  35397 MW;  F5AA7286F3A40ABE CRC64;

  Query Match             61.6%;  Score 992;  DB 11;  Length 313;
  Best Local Similarity   60.6%;  Pred. No. 1.9e-81;
  Matches  183;  Conservative   47;  Mismatches   72;  Indels    0;  Gaps    0;

Qy          4 LNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMYFFL 63
              :||| |  |    ||: |  ::|  |  |    |:||| |||||::  :    |||||||||
Db          7 INQTSVMSFRLTGLSTNPKVQMAIFFIFLIFYVLTLVGNILIVVTIIHDHRLHTPMYFFL 66

Qy         64 SNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAYDRY 123
              |||||||:|||:|||||||      | | ||||:|: |:||||||| |||||  ::|||||
Db         67 SNLSFIDVCHSTVTVPKMLSDTFSEEKLISFDDCVVQIFFLHLFACTEIFLLTVMAYDRY 126

Qy        124 VAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCDVPL 183
              |||| || |  :|| :||: |  |:|  ||:||:  | |||:|||||: ||::|||||
Db        127 VAICKPLRYMTIMNWKVCMVLGGAMWTAGTIHSISFTSLTIKLPYCGPNELDSFFCDVPQ 186

Qy        184 VIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTCSAH 243
              ||:|||||| :| ||:|:||| ||: ||: : || |||||||:  ::|::|||||:||
Db        187 VIELACTDTRITEILVVSNSGMISMVCFVIIVVSYAVILVSLRQQISDGKRKALSTCAAH 246

Qy        244 FMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQLRQ 303
                || || | |||||:|| |   ||:|| |:| :|||||| ||| |||::|||:|:| :
Db        247 LTVVTLFLGHCIFIYSRPAISLPEDKIVSAFFTAITPLLNPIIYTFRNEDMKSALKKLIR 306

Qy        304 RQ 305
              |:
Db        307 RK 308


RESULT 6
Q8NH73
ID   Q8NH73      PRELIMINARY;      PRT;   311 AA.
AC   Q8NH73;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Seven transmembrane helix receptor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
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RN   [1]
RP   SEQUENCE FROM N.A.
RA   Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA   Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RT   "Genome-wide discovery and analysis of human seven transmembrane helix
RT   receptor genes.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB065516; BAC05764.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor; Transmembrane.
SQ   SEQUENCE   311 AA;  35138 MW;  8EAA48E9C3B081BC CRC64;

  Query Match             58.2%;  Score 938;  DB 4;  Length 311;
  Best Local Similarity   55.4%;  Pred. No. 1.4e-76;
  Matches  170;  Conservative   59;  Mismatches   76;  Indels    2;  Gaps    1;

Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              |: :|   ||||:| ||: :  :| : |: ||  |:: | ||:||::    :    :|||
Db          1 MEKIN--NVTEFIFWGLSQSPEIEKVCFVVFSFFYIIILLGNLLIMLTVCLSNLFKSPMY 58

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
              |||| |||:|||:|||| |||:  || : ||||:  |: ||  :| | | |||:| ::||
Db         59 FFLSFLSFVDICYSSVTAPKMIVDLLAKDKTISYVGCMLQLLGVHFFGCTEIFILTVMAY 118

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
              ||||||| |||| :||   | :::   |:|| :||: |  | ::||:|||| || ||||
Db        119 DRYVAICKPLHYMTIMNRETCNKMLLGTWVGGFLHSIIQVALVVQLPFCGPNEIDHYFCD 178

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTC 240
              |  |:|||||:||: |:::  |||||:|  |: :: || :|||||| |||||:||||||
Db        179 VHPVLKLACTETYIVGVVVTANSGTIALGSFVILLISYSIILVSLRKQSAEGRRKALSTC 238

Qy        241 SAHFMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300
               :|  :| :||||| |:| ||||:|| ||:|:||||::||:||| |||||| |||:|||:
Db        239 GSHIAMVVIFFGPCTFMYMRPDTTFSEDKMVAVFYTIITPMLNPLIYTLRNAEVKNAMKK 298

Qy        301 LRQRQVF 307
              |  | ||
Db        299 LWGRNVF 305


RESULT 7
Q8VF96
ID   Q8VF96      PRELIMINARY;      PRT;   318 AA.
AC   Q8VF96;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Olfactory receptor MOR226-1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zhang X., Firestein S.J.;
RT   "The olfactory receptor gene superfamily of the mouse.";
RL   Nat. Neurosci. 0:0-0(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Adams M.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY073638; AAL61301.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   318 AA;  36298 MW;  621BDE95D4CAA826 CRC64;

  Query Match             57.8%;  Score 931;  DB 11;  Length 318;
  Best Local Similarity   55.7%;  Pred. No. 6.1e-76;
  Matches  170;  Conservative   58;  Mismatches   75;  Indels    2;  Gaps    1;

Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              |: :|   ||||:|||: |  :| : |: ||  ||: | ||:||::          |||
Db          8 MEEVN--NVTEFIFLGLSQNPEVEKVCFVVFSFFYMVILLGNLLIMLTVCSGNLFKFPMY 65

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
              ||: |||:|||:|||| |||:  ||:::||||:  |: ||| :| | | |||:| ::||
Db         66 FFLNFLSFVDICYSSVTAPKMIIDLLVKKKTISYVGCMLQLFVVHFFGCTEIFILTVMAY 125

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
              ||||||| |||| :|:   | :::   |:|| :||: |  | ::||:|||| || ||||
Db        126 DRYVAICKPLHYMTIMDRERCNKMLLGTWIGGFLHSIIQVALVVQLPFCGPNEIDHYFCD 185

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTC 240
              |  |:|||||||: || :  |||||:|  |: :: || |||:|||| |:|||:||||||
Db        186 VHPVLKLACTDTYIVGIFVTANSGTIALGSFVILLISYTVILMSLRKQSSEGRRKALSTC 245

Qy        241 SAHFMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300
               :|  || :||||| |:| ||||:|| ||:|: |||::||:||| |||||| |||:||::
Db        246 GSHIAVVIIFFGPCTFMYMRPDTTFSEDKMVATFYTIITPMLNPLIYTLRNAEVKNAMRK 305

Qy        301 LRQRQ 305
              |  |:
Db        306 LWARK 310


RESULT 8
Q8NGD2
ID   Q8NGD2      PRELIMINARY;      PRT;   314 AA.
AC   Q8NGD2;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Seven transmembrane helix receptor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA   Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RT   "Genome-wide discovery and analysis of human seven transmembrane helix
RT   receptor genes.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB065883; BAC06101.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor; Transmembrane.
SQ   SEQUENCE   314 AA;  35357 MW;  946877CDB260EC59 CRC64;

  Query Match             57.7%;  Score 929;  DB 4;  Length 314;
  Best Local Similarity   53.1%;  Pred. No. 9.1e-76;
  Matches  165;  Conservative   67;  Mismatches   79;  Indels    0;  Gaps    0;

Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              ||  |:: ::||| |||::  |:| ||| || :|: |: || ||:|  :  | ||:|||
Db          1 MDVGNKSTMSEFVLLGLSNSWELQMFFFMVFSLLYVATMVGNSLIVITVIVDPHLHSPMY 60

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
              | |:||| ||:  :|   |||:   |   |||||| |:||:|||||   || ||: :::
Db         61 FLLTNLSIIDMSLASFATPKMITDYLTGHKTISFDGCLTQIFFLHLFTGTEIILLMAMSF 120

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
              |||:||| |||| :|:: :||: || | |: | :||: |    : ||:|||  :||:|||
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```
Db        121 DRYIAICKPLHYASVISPQVCVALVVASWIMGVMHSMSQVIFALTLPFCGPYEVDSFFCD 180

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTC 240
              :|:| :||| |||: |: ::: || |:||||: :  ||:::||:::||: |  ||||||
Db        181 LPVVFQLACVDTYVLGLFMISTSGIIALSCFIVLFNSYVIVLVTVKHHSSRGSSKALSTC 240

Qy        241 SAHFMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300
              :|||:|| |||||||||| | :||  ||::|||||: || ||| |||||:||| ||::
Db        241 TAHFIVVFLFFGPCIFIYMWPLSSFLTDKILSVFYTIFTPTLNPIIYTLRNQEVKIAMRK 300

Qy        301 LRQRQVFFTKS 311
              |: | : | |:
Db        301 LKNRFLNFNKA 311


RESULT 9
Q8NGD5
ID   Q8NGD5      PRELIMINARY;      PRT;   310 AA.
AC   Q8NGD5;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Seven transmembrane helix receptor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA   Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RT   "Genome-wide discovery and analysis of human seven transmembrane helix
RT   receptor genes.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB065880; BAC06098.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor; Transmembrane.
SQ   SEQUENCE   310 AA;  35052 MW;  AA7B06959BFE8E0D CRC64;

  Query Match             57.6%;  Score 927.5;  DB 4;  Length 310;
  Best Local Similarity   55.0%;  Pred. No. 1.2e-75;
  Matches  170;  Conservative   60;  Mismatches   78;  Indels    1;  Gaps    1;

Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLH-TPM 59
              ||  | : |:||| ||  :| |:  ||: |  :|:  : ||:||:: :  | || :||
Db          1 MDPQNYSLVSEFVLHGLCTSRHLQNFFFIFFFGVYVAIMLGNLLILVTVISDPCLHSSPM 60

Qy         60 YFFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVA 119
              || | ||:|:|:  :|   |||:   | ::| |||  |: |:|||   ||: ||: :|
Db         61 YFLLGNLAFLDMWLASFATPKMIRDFLSDQKLISFGGCMAQIFFLHFTGGAEMVLLVSMA 120

Qy        120 YDRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFC 179
              |||||||| |||| :|: : ||:|| | |: | |||: |   |: |||||| :||:||
Db        121 YDRYVAICKPLHYMTLMSWQTCIRLVLASWVVGFVHSISQVAFTVNLPYCGPNEVDSFFC 180

Qy        180 DVPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALST 239
              |:|||||||| |||: ||:::::|| :|||||| :: || |||:::|: :|    |||||
Db        181 DLPLVIKLACMDTYVLGIIMISDSGLLSLSCFLLLLISYTVILLAIRQRAAGSTSKALST 240

Qy        240 CSAHFMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMK 299
              |||| ||| |||||||:| || : ||:||::|||||: |||||| ||||||||:|:|||
Db        241 CSAHIMVVTLFFGPCIFVYVRPFSRFSVDKLLSVFYTIFTPLLNPIIYTLRNEEMKAAMK 300

Qy        300 QLRQRQVFF 308
              :|: |:| |
Db        301 KLQNRRVTF 309


RESULT 10
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Q8VGN8
ID   Q8VGN8      PRELIMINARY;      PRT;   308 AA.
AC   Q8VGN8;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Olfactory receptor MOR227-3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zhang X., Firestein S.J.;
RT   "The olfactory receptor gene superfamily of the mouse.";
RL   Nat. Neurosci. 0:0-0(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Adams M.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY073108; AAL60771.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   308 AA;  34374 MW;  BE466A13B5D05116 CRC64;

  Query Match             57.2%;  Score 921;  DB 11;  Length 308;
  Best Local Similarity   55.2%;  Pred. No. 4.7e-75;
  Matches  164;  Conservative   60;  Mismatches   73;  Indels    0;  Gaps    0;

Qy          5 NQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMYFFLS 64
              |:  :|| :| ||  :  :: : |: |  :|: || || ||::|   : :||:|||||||
Db          3 NKNNITELIFTGLFQDPEVQKVCFVLFLPVYLATLLGNSLIVVAVSISKTLHSPMYFFLS 62

Qy         65 NLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAYDRYV 124
              :|| ::||:|| ||| :  ||:: |||| |: |:|| |    ||| ||:::||||||
Db         63 SLSLVEICYSSTIVPKFITDLLVKVKTISLKGCLAQIFFSHFLGVAEILLLVVMAYDRYV 122

Qy        125 AICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCDVPLV 184
              ||| |||| |:|: :||  ||  |||| :||: |  :|| ||:||||:|| ||||:  :
Db        123 AICKPLHYMNIMSRQVCHMLVGGSWLGGLIHSIIQIIITIPLPFCGPNVIDHYFCDLQPL 182

Qy        185 IKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTCSAHF 244
              |||||||:: |:::: ||| ||:     :|:|| :||:|||||||||:||||||::|
Db        183 FKLACTDTFMEGVVVMANSGLISIISLFILVSSYAIILISLRKHSAEGRRKALSTCASHI 242

Qy        245 MVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQL 301
              || |||||  |:| || :||: ||:|:|||||:||:||| |||||| |||:|||:|
Db        243 TVVILFFGPATFLYLRPSSSFTEDKLVAVFYTVITPMLNPIIYTLRNAEVKNAMKKL 299


RESULT 11
Q8VF11
ID   Q8VF11      PRELIMINARY;      PRT;   326 AA.
AC   Q8VF11;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Olfactory receptor MOR246-5.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zhang X., Firestein S.J.;
RT   "The olfactory receptor gene superfamily of the mouse.";
RL   Nat. Neurosci. 0:0-0(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
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RA   Adams M.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY073730; AAL61393.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR000985; Lectin_legA.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
DR   PROSITE; PS00308; LECTIN_LEGUME_ALPHA; 1.
KW   Receptor.
SQ   SEQUENCE   326 AA;  37023 MW;  DE2E1F4FB7B4EFC5 CRC64;

  Query Match             57.1%;  Score 920;  DB 11;  Length 326;
  Best Local Similarity   53.7%;  Pred. No. 6.1e-75;
  Matches  165;  Conservative   61;  Mismatches   81;  Indels    0;  Gaps    0;

Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              |: || :|| ||| ||||:  |:: ||:|||  |::|: || ||:   : |  ||:||:
Db          1 MERLNHSRVPEFVLLGLTDSPELQIFFFVAFSIFYLMTMLGNCLILFTVLSTSHLHSPMF 60

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
              | ||||| |||| ||   |||:       |||||: ||:|:| ||||    || ||| :::
Db         61 FLLSNLSLIDICLSSFATPKMIMDFFAHHKTISFEGCISQIFLLHLFTGTEIVLLISMSF 120

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
              |||:||| ||:|  :|: :||: || | |: | :|:: |    : ||:||||::||:|||
Db        121 DRYIAICKPLYYSTIMSQKVCVGLVIASWMVGFLHTMSQLVFILYLPFCGPNVVDSFFCD 180

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTC 240
              :||||:||| |||: |: :|  || |:|  || :: ||:|:||::| ||: |  ||||||
Db        181 LPLVIQLACIDTYVLGVFMVATSGVIALISFLLLLISYIVVLVTIRGHSSIGSSKALSTC 240

Qy        241 SAHFMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300
              ::|| || :|||||| ||  | |:| :||::|||||: || ||| ||||||:||::|:|:
Db        241 TSHFTVVLMFFGPCILIYVWPFTNFLMDKILSVFYTIFTPFLNPLIYTLRNQEVRTAVKK 300

Qy        301 LRQRQVF 307
                  | |
Db        301 KISNQYF 307


RESULT 12
Q8NH41
ID   Q8NH41      PRELIMINARY;      PRT;   324 AA.
AC   Q8NH41;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Seven transmembrane helix receptor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA   Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RT   "Genome-wide discovery and analysis of human seven transmembrane helix
RT   receptor genes.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB065560; BAC05798.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR000985; Lectin_legA.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
DR   PROSITE; PS00308; LECTIN_LEGUME_ALPHA; 1.
KW   Receptor; Transmembrane.
SQ   SEQUENCE   324 AA;  36483 MW;  76AC2F465AA07A9F CRC64;

  Query Match             57.0%;  Score 919;  DB 4;  Length 324;
  Best Local Similarity   56.2%;  Pred. No. 7.4e-75;
  Matches  171;  Conservative   50;  Mismatches   83;  Indels    0;  Gaps    0;

Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              |:  | :|||||| |||: :| |:   |: || :|:  | || |||:       ||||||
Db          1 MNETNHSRVTEFVLLGLSSSRELQPFLFLTFSLLYLAILLGNFLIILTVTSDSRLHTPMY 60

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
              | |:||||||:| :|   |||:   |:||||||| |: |:||:|||  :|: ||: :||
Db         61 FLLANLSFIDVCVASFATPKMIADFLVERKTISFDACLAQIFFVHLFTGSEMVLLVSMAY 120

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
              |||||| |||| ||: |||: ||   |  | :|:  |   |: ||:|||| :||:|||
Db        121 DRYVAICKPLHYMTVMSRRVCVVLVLISWFVGFIHTTSQLAFTVNLPFCGPNKVDSFFCD 180

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTC 240
              :||| |||| |||:  :||| :|| :||| || :| || ||||::|  |:    || ||
Db        181 LPLVTKLACIDTYVVSLLIVADSGFLSLSSFLLLVVSYTVILVTVRNRSSASMAKARSTL 240

Qy        241 SAHFMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300
              :||  || ||||||||||  | :|:|:|||::|||: | :||| ||||||:|||:|| :
Db        241 TAHITVVTLFFGPCIFIYVWPFSSYSVDKVLAVFYTIFTLILNPVIYTLRNKEVKAAMSK 300

Qy        301 LRQR 304
              |: |
Db        301 LKSR 304


RESULT 13
Q8VEZ3
ID   Q8VEZ3      PRELIMINARY;      PRT;   309 AA.
AC   Q8VEZ3;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Olfactory receptor MOR228-2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zhang X., Firestein S.J.;
RT   "The olfactory receptor gene superfamily of the mouse.";
RL   Nat. Neurosci. 0:0-0(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Adams M.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY073750; AAL61413.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   309 AA;  34586 MW;  7D9DADA3145BCAF9 CRC64;

  Query Match             57.0%;  Score 918;  DB 11;  Length 309;
  Best Local Similarity   57.0%;  Pred. No. 8.7e-75;
  Matches  167;  Conservative   54;  Mismatches   72;  Indels    0;  Gaps    0;

Qy          9 VTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMYFFLSNLSF 68
              ||||:|||: |: :|:: |: |  :||  : ||:|:::  | : || :|||||  |||
Db          7 VTEFLFLGLSSNKEVEIVCFVIFLLLYMAIVLGNLLMVVTVVASRSLGSPMYFFLGYLSF 66

Qy         69 IDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAYDRYVAICT 128
              ::||:|| | ||::  || |:|:||   |:|||||:| |  |||||| ::||||||||
Db         67 VEICYSSTTAPKLILDLLAEKKSISVWGCMTQLFFMHFFGGAEIFLLTVMAYDRYVAICK 126

Qy        129 PLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCDVPLVIKLA 188
              |||| ::||  ||  ||   |:|| |||  |  |   ||:|||||| ||||:  ::|||
Db        127 PLHYTSIMNRNVCAVLVGTAWIGGFVHSFAQILLIFPLPFCGPNIIDHYFCDLLPLLKLA 186
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Qy        189 CTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTCSAHFMVVA 248
              |:||:| |:||| |:||:|:  |: :: ||:|||  ||  |||||:|||||| :|  ||
Db        187 CSDTFLIGLLIVANAGTLSVISFVVLLASYVVILFHLRTQSAEGRRKALSTCGSHVTVVI 246

Qy        249 LFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQL 301
              ||||||:||| ||  :  :||:::|||||:|||||| ||:||| :||  || |
Db        247 LFFGPCVFIYLRPSDTLPVDKMIAVFYTVITPLLNPLIYSLRNAKVKKTMKSL 299


RESULT 14
Q8VEX0
ID   Q8VEX0      PRELIMINARY;      PRT;   321 AA.
AC   Q8VEX0;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Olfactory receptor MOR246-4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zhang X., Firestein S.J.;
RT   "The olfactory receptor gene superfamily of the mouse.";
RL   Nat. Neurosci. 0:0-0(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Adams M.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY073777; AAL61440.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR000985; Lectin_legA.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
DR   PROSITE; PS00308; LECTIN_LEGUME_ALPHA; 1.
KW   Receptor.
SQ   SEQUENCE   321 AA;  36286 MW;  A1BCFDD8E61B798D CRC64;

  Query Match             56.7%;  Score 914;  DB 11;  Length 321;
  Best Local Similarity   55.6%;  Pred. No. 2.1e-74;
  Matches  169;  Conservative   51;  Mismatches   84;  Indels    0;  Gaps    0;

Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              |:  | :|||||| |||: :: |:   |: || :|:  | || |||:     | ||||||
Db          1 MNERNYSRVTEFVLLGLSSSKELQPFLFLIFSLLYLAILLGNFLIILTVTSDPRLHTPMY 60

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
              | |:|||||:| :|   ||||   |:|||||: |: |:| :| || |: ||: :||
Db         61 FLLANLSFIDMCVASFATPKMLADFLVERKTISFEACLAQIFCVHQFAGGEMVLLVSMAY 120

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
              ||||||| |||| :|: |||| ||   | | :|:: |   |: ||:|||| :||:|||
Db        121 DRYVAICKPLHYMTIMSRRVCITLVIIPWFVGFIHTMSQLAFTVNLPFCGPNQVDSFFCD 180

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTC 240
              :||| ||||||||   :||| :|| ::|| |: :| || |||:::|  |:    || ||
Db        181 LPLVTKLACTDTYFVSLLIVADSGVLTLSTFVFLVISYTVILITVRNRSSASMAKARSTL 240

Qy        241 SAHFMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300
              :||  || ||||||||||  |   :|:|||::||||: ||:||| |||||:|||:|| :
Db        241 TAHITVVVLFFGPCIFIYAWPFNGYSVDKVLAVFYTIFTPILNPLIYTLRNKEVKAAMSK 300

Qy        301 LRQR 304
              || |
Db        301 LRGR 304


RESULT 15
Q8VEX3
ID   Q8VEX3      PRELIMINARY;      PRT;   324 AA.
AC   Q8VEX3;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Olfactory receptor MOR246-2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zhang X., Firestein S.J.;
RT   "The olfactory receptor gene superfamily of the mouse.";
RL   Nat. Neurosci. 0:0-0(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Adams M.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY073774; AAL61437.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR000985; Lectin_legA.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
DR   PROSITE; PS00308; LECTIN_LEGUME_ALPHA; 1.
KW   Receptor.
SQ   SEQUENCE   324 AA;  36535 MW;  8D2BB4086766F0BA CRC64;

  Query Match             56.6%;  Score 912;  DB 11;  Length 324;
  Best Local Similarity   55.9%;  Pred. No. 3.2e-74;
  Matches  170;  Conservative   51;  Mismatches   83;  Indels    0;  Gaps    0;

Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              |:  | :|||||| |||: :: |:   |: || :|:  | || |||:     | ||||||
Db          1 MNETNYSRVTEFVLLGLSSSKELQPFLFLIFSLLYLAILLGNFLIILTVTSDPRLHTPMY 60

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
              | |:|||||:| :|   ||||   |:|||||: |: |:||:|||   |: ||: :||
Db         61 FLLANLSFIDMCVASFATPKMLADFLVERKTISFEACLAQIFFVHLFTGGEMVLLVSMAY 120

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
              ||||||| |||| :|: |||| ||   | | :|:  |   |: ||:|||| :||:|||
Db        121 DRYVAICKPLHYMTIMSRRVCIILVCISWFVGFIHTTSQLAFTVNLPFCGPNKVDSFFCD 180

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTC 240
              : || |||| |||:  :||| :|| :|:| || :| || |||:::|  |:    || ||
Db        181 LLLVTKLACIDTYVVSLLIVADSGFLSMSSFLLLVVSYTVILITVRNRSSASMAKARSTL 240

Qy        241 SAHFMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300
              :||  || ||||||||||  | :|:|:|||::||||: ||:||| |||||:|||:|| :
Db        241 TAHITVVVLFFGPCIFIYVWPFSSYSVDKVLAVFYTIFTPILNPVIYTLRNKEVKAAMSK 300

Qy        301 LRQR 304
              || |
Db        301 LRGR 304


Search completed: August 12, 2003, 16:09:00
Job time : 99 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 12, 2003, 15:29:51 ; Search time 23 Seconds
(without alignments)
639.972 Million cell updates/sec

Title: US-09-807-132-4
Perfect score: 1611
Sequence: 1 MDSLNQTRVTEFVFLGLTDN.....VKSAMKQLRQRQVFFTKSYT 313

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	839	52.1	310	1	O4D1_HUMAN	Q15615 homo sapien
2	813.5	50.5	307	1	O4D2_HUMAN	P58180 homo sapien
3	781	48.5	312	1	O4F3_HUMAN	O95013 homo sapien
4	727.5	45.2	321	1	O5V1_HUMAN	Q9ugf6 homo sapien
5	702.5	43.6	312	1	O1F1_HUMAN	O43749 homo sapien
6	694.5	43.1	314	1	O5I1_HUMAN	Q13606 homo sapien
7	693	43.0	311	1	OLF1_CANFA	Q95154 canis famil
8	689	42.8	307	1	OCD2_HUMAN	P58182 homo sapien
9	686.5	42.6	308	1	O2D2_HUMAN	Q9h210 homo sapien
10	686.5	42.6	313	1	OLF5_RAT	P23266 rattus norv
11	681.5	42.3	312	1	OAC1_HUMAN	Q96kk4 homo sapien
12	681	42.3	316	1	OCD3_HUMAN	Q9ugf7 homo sapien
13	677.5	42.1	314	1	O5BG_HUMAN	Q96r08 homo sapien
14	676.5	42.0	320	1	O7C1_HUMAN	O76099 homo sapien
15	675	41.9	314	1	O1Q1_HUMAN	Q15612 homo sapien
16	674.5	41.9	309	1	O7AA_HUMAN	O76100 homo sapien
17	674.5	41.9	333	1	OLF3_RAT	P23265 rattus norv
18	670.5	41.6	308	1	O8D1_HUMAN	Q8wz84 homo sapien
19	668.5	41.5	314	1	O5F1_HUMAN	O95221 homo sapien
20	667.5	41.4	309	1	OLF4_CANFA	Q95157 canis famil
21	665	41.3	315	1	OAA4_HUMAN	Q9h209 homo sapien
22	664.5	41.2	313	1	O1G1_HUMAN	P47890 homo sapien
23	662.5	41.1	311	1	O5P3_HUMAN	Q8wz94 homo sapien
24	661.5	41.1	310	1	OLF0_RAT	P23269 rattus norv
25	660	41.0	313	1	O2B6_HUMAN	P58173 homo sapien
26	660	41.0	327	1	OLF7_RAT	P23270 rattus norv
27	659.5	40.9	312	1	OL15_MOUSE	P23275 mus musculu
28	658.5	40.9	314	1	OLF9_RAT	P23272 rattus norv
29	656	40.7	314	1	O1E1_HUMAN	P30953 homo sapien
30	656	40.7	314	1	OLF1_RAT	P23274 rattus norv
31	655	40.7	313	1	OLFD_CANFA	P30955 canis famil
32	653.5	40.6	311	1	O6B1_HUMAN	O95007 homo sapien
33	653.5	40.6	312	1	OLF4_RAT	P23273 rattus norv
34	652.5	40.5	309	1	O5B2_HUMAN	Q96r09 homo sapien
35	648.5	40.3	312	1	O2C1_HUMAN	O95371 homo sapien
36	648.5	40.3	313	1	O1C1_HUMAN	Q15619 homo sapien
37	645	40.0	317	1	OAA5_HUMAN	Q9h207 homo sapien
38	644.5	40.0	312	1	O2J2_HUMAN	O76002 homo sapien
39	644.5	40.0	319	1	O7A5_HUMAN	Q15622 homo sapien
40	643	39.9	313	1	O2B3_HUMAN	O76000 homo sapien
41	641.5	39.8	309	1	O7AH_HUMAN	O14581 homo sapien
42	640.5	39.8	317	1	OLF3_CANFA	Q95156 canis famil
43	638.5	39.6	312	1	OLF8_RAT	P23271 rattus norv
44	637.5	39.6	357	1	O2B2_HUMAN	Q9gzk3 homo sapien
45	634.5	39.4	311	1	O2J3_HUMAN	O76001 homo sapien

ALIGNMENTS

```
RESULT 1
O4D1_HUMAN
ID   O4D1_HUMAN      STANDARD;      PRT;   310 AA.
AC   Q15615;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Olfactory receptor 4D1 (Olfactory receptor TPCR16).
GN   OR4D1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE OF 126-279 FROM N.A.
RC   TISSUE=Testis;
RX   MEDLINE=97224452; PubMed=9119360;
RA   Vanderhaeghen P., Schurmans S., Vassart G., Parmentier M.;
RT   "Specific repertoire of olfactory receptor genes in the male germ
RT   cells of several mammalian species.";
RL   Genomics 39:239-246(1997).
CC   -!- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X89670; CAA61817.1; -.
DR   PIR; S58015; S58015.
DR   Genew; HGNC:8293; OR4D1.
DR   GO; GO:0016021; C:integral to membrane; NAS.
DR   GO; GO:0004984; F:olfactory receptor activity; NAS.
DR   GO; GO:0007608; P:olfaction; NAS.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Olfaction.
FT   DOMAIN        1     25       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     26     49       1 (POTENTIAL).
FT   DOMAIN       50     57       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     58     79       2 (POTENTIAL).
FT   DOMAIN       80    100       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    101    120       3 (POTENTIAL).
FT   DOMAIN      121    139       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    140    158       4 (POTENTIAL).
FT   DOMAIN      159    195       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    196    219       5 (POTENTIAL).
```

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FT   DOMAIN      220    235       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    236    258       6 (POTENTIAL).
FT   DOMAIN      259    269       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    270    289       7 (POTENTIAL).
FT   DOMAIN      290    310       CYTOPLASMIC (POTENTIAL).
FT   DISULFID     97    189       BY SIMILARITY.
FT   CARBOHYD      5      5       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   310 AA;  35358 MW;  076DCD28B16F70EC CRC64;

  Query Match             52.1%;  Score 839;  DB 1;  Length 310;
  Best Local Similarity   50.8%;  Pred. No. 3.5e-56;
  Matches  153;  Conservative   60;  Mismatches   88;  Indels    0;  Gaps    0;

Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              |:  | |:|: || || :  : |:   |: |  :|: |: ||:||::   |   ||||||
Db          1 MEPQNTTQVSMFVLLGFSQTQELQKFLFLLFLLVYVTTIVGNLLIMVTVTFDCRLHTPMY 60

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
              | | ||: ||:|:|:|| ||||   | | ||||:  |: |:|| ||     :| | ::||
Db         61 FLLRNLALIDLCYSTVTSPKMLVDFLHETKTISYQGCMAQIFFFHLLGGGTVFFLSVMAY 120

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
              |||:||  || |  :|| ::|: || | |:|| |||: |  | : ||:| |||||:::||
Db        121 DRYIAISQPLRYVTIMNTQLCVGLVVAAWVGGFVHSIVQLALILPLPFCDPNIIDNFYCD 180

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTC 240
              || |::|||||| |   |:: ||| : :  || :: || |||| || || : |:|| |||
Db        181 VPQVLRLACTDTSLLEFLMIFNSGLLVIIWFLLLLISYTVILVMLRSHSGKARRKAASTC 240

Qy        241 SAHFMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300
              : | :||:: | |||:||| | | | :|| ||: |||:||:||| ||||||:::|:||::
Db        241 TTHIIVVSMIFIPCIYIYTWPFTPFLMDKAVSISYTVMTPMLNPMIYTLRNQDMKAAMRR 300

Qy        301 L 301
              |
Db        301 L 301


RESULT 2
O4D2_HUMAN
ID   O4D2_HUMAN     STANDARD;      PRT;   307 AA.
AC   P58180;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Olfactory receptor 4D2.
GN   OR4D2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Birren B., Linton L., Nusbaum C., Lander E.;
RL   Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AC005962; -; NOT_ANNOTATED_CDS.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Olfaction.
FT   DOMAIN        1     25       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     26     49       1 (POTENTIAL).
FT   DOMAIN       50     57       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     58     79       2 (POTENTIAL).
FT   DOMAIN       80    100       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    101    120       3 (POTENTIAL).
FT   DOMAIN      121    139       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    140    158       4 (POTENTIAL).
FT   DOMAIN      159    195       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    196    219       5 (POTENTIAL).
FT   DOMAIN      220    235       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    236    258       6 (POTENTIAL).
FT   DOMAIN      259    269       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    270    289       7 (POTENTIAL).
FT   DOMAIN      290    307       CYTOPLASMIC (POTENTIAL).
FT   DISULFID     97    189       BY SIMILARITY.
FT   CARBOHYD      5      5       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   307 AA;  34958 MW;  5C8C68269034EBD3 CRC64;

  Query Match             50.5%;  Score 813.5;  DB 1;  Length 307;
  Best Local Similarity   49.8%;  Pred. No. 2.9e-54;
  Matches  153;  Conservative   63;  Mismatches   90;  Indels    1;  Gaps    1;

Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              |:: | | |::|||||:  | |:   |: |  :|: |: |||||||       ||||||
Db          1 METGNLTWVSDFVFLGLSQTRELQRFLFLMFLFVYITTVMGNILIIITVTSDSQLHTPMY 60

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
              | | ||: :|:| |||| ||||   || |:||||:  |: |:|| |     | :| | ::|:
Db         61 FLLRNLAVLDLCFSSVTAPKMLVDLLSEKKTISYQGCMGQIFFFHFLGGAMVFFLSVMAF 120

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
              || :|| || |  ||| :: : || | |:|| |||: |  | : ||:|||||:|:::||
Db        121 DRLIAISRPLRYVTVMNTQLWVGLVVATWVGGFVHSIVQLALMLPLPFCGPNILDNPYCD 180

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTC 240
              || |::|||||| |   | ::||| : :  |  :: ||: ||| || |  | |:|| |||
Db        181 VPQVLRLACTDTSLLEFLKISNSGLLDVVWFFLLLMSYLFILVMLRSHPGEARRKAASTC 240

Qy        241 SAHFMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300
              : | :||:: | | |::| || | | :||:||: :||:||:||| ||||||:::::|:::
Db        241 TTHIIVVSMIFVPSIYLYARPFTPFPMDKLVSIGHTVMTPMLNPMIYTLRNQDMQAAVRR 300

Qy        301 L-RQRQV 306
              | | | |
Db        301 LGRHRLV 307


RESULT 3
O4F3_HUMAN
ID   O4F3_HUMAN     STANDARD;      PRT;   312 AA.
AC   O95013;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Olfactory receptor 4F3.
GN   OR4F3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Courtney L., Langston Y., Stoneking T., Drone K., Shih K.;
RL   Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; AC004908; AAD05195.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Olfaction.
FT   DOMAIN        1     25       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     26     49       1 (POTENTIAL).
FT   DOMAIN       50     57       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     58     79       2 (POTENTIAL).
FT   DOMAIN       80    100       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    101    120       3 (POTENTIAL).
FT   DOMAIN      121    139       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    140    158       4 (POTENTIAL).
FT   DOMAIN      159    195       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    196    219       5 (POTENTIAL).
FT   DOMAIN      220    235       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    236    258       6 (POTENTIAL).
FT   DOMAIN      259    269       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    270    289       7 (POTENTIAL).
FT   DOMAIN      290    312       CYTOPLASMIC (POTENTIAL).
FT   DISULFID     97    189       BY SIMILARITY.
FT   CARBOHYD      5      5       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   312 AA;  35087 MW;  ABEE3F4AABA43F86 CRC64;

  Query Match             48.5%;  Score 781;  DB 1;  Length 312;
  Best Local Similarity   45.8%;  Pred. No. 7.9e-52;
  Matches  142;  Conservative   71;  Mismatches   97;  Indels    0;  Gaps    0;

Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              ||  | : |:||:||||| :  :::|  :  | :|: :::|||||: :    | ||:|||
Db          1 MDGENHSVVSEFLFLGLTHSWEIQLLLLVFSSVLYVASITGNILIVFSVTTDPHLHSPMY 60

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
              | |::|||||:   ||| |||:  |  :|| |||  || |:||:|:   |: ||| :|:
Db         61 FLLASLSFIDLGACSVTSPKMIYDLFRKRKVISFGGCIAQIFFIHVIGGVEMVLLIAMAF 120

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
              |||||:| ||||  :|: |:|:  :    |  |||  |   : | :||||::||::||
Db        121 DRYVALCKPLHYLTIMSPRMCLSFLAVAWTLGVSHSLFQLAFLVNLAFCGPNVLDSFYCD 180

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTC 240
              :| :::|||||||    ::  ||| | :  |  :: ||: || :: |||: |  |||||
Db        181 LPRLLRLACTDTYRLQFMVTVNSGFICVGTFFILLISYVFILFTVWKHSSGGSSKALSTL 240

Qy        241 SAHFMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300
              |||  || ||||| :|:|||  :  :|| :::|  |:|| ||| :|| ||:|:|:|:|:
Db        241 SAHSTVVLLFFGPPMFVYTRPHPNSQMDKFLAIFDAVLTPFLNPVVYTFRNKEMKAAIKR 300

Qy        301 LRQRQVFFTK 310
              : :: | : :
Db        301 VCKQLVIYKR 310


RESULT 4
O5V1_HUMAN
ID   O5V1_HUMAN     STANDARD;      PRT;   321 AA.
AC   Q9UGF6;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Olfactory receptor 5V1 (Hs6M1-21).
GN   OR5V1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Tracey A.;
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------------
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CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; AL096770; CAB65797.1; -.
DR   Genew; HGNC:13972; OR5V1.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Olfaction.
FT   DOMAIN        1     25       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     26     49       1 (POTENTIAL).
FT   DOMAIN       50     57       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     58     79       2 (POTENTIAL).
FT   DOMAIN       80    100       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    101    120       3 (POTENTIAL).
FT   DOMAIN      121    139       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    140    158       4 (POTENTIAL).
FT   DOMAIN      159    195       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    196    219       5 (POTENTIAL).
FT   DOMAIN      220    236       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    237    259       6 (POTENTIAL).
FT   DOMAIN      260    272       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    273    292       7 (POTENTIAL).
FT   DOMAIN      293    321       CYTOPLASMIC (POTENTIAL).
FT   DISULFID     97    189       BY SIMILARITY.
FT   CARBOHYD      5      5       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   321 AA;  36056 MW;  AAC426FDCF58E375 CRC64;

  Query Match             45.2%;  Score 727.5;  DB 1;  Length 321;
  Best Local Similarity   45.7%;  Pred. No. 8.3e-48;
  Matches  139;  Conservative   67;  Mismatches   95;  Indels    3;  Gaps    2;

Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              |:  ||| :|||: || ::   |: | |  |   |  || ||||||: ||  | ||||||
Db          1 MERKNQTAITEFIILGFSNLNELQFLLFTIFFLTYFCTLGGNILIILLTTVTDPHLHTPMY 60

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
              :|| ||:|||||::   ||:|:  || ::|:||:  |: |||     |  :|  ||  :||
Db         61 YFLGNLAFIDICYTTSNVPQMMVHLLSKKKSISYVGCVVQLFAFVFFVGSECLLLAAMAY 120

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
              |||:||| || |  :::  :| ||  : |  | ::|:  | ||  ||:|| | |: :|||
Db        121 DRYIAICNPLRYSVILSKVLCNQLAASCWAAGFLNSVVHTVLTFCLPFCGNNQINYFFCD 180

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVS-LRKHSAEGRQKALST 239
              :| :: |:| :| :  : :::    |  : || :| ||: |: : ||  |:|||:|| ||
Db        181 IPPLLILSCGNTSVNELALLSTGVFIGWTPFLCIVLSYICIISTILRIQSSEGRRKAFST 240

Qy        240 CSAHFMVVALFFGPCIFIYTRPDTSFSI--DKVVSVFYTVVTPLLNPFIYTLRNEEVKSA 297
              |::| :| ||:|  || | ||:::|:  |::||| |:||||:||| ||||||:::| |
Db        241 CASHLAIVFLFYGSAIFTYVRPISTYSLKKDRLVSVLYSVVTPMLNPIIYTLRNKDIKEA 300

Qy        298 MKQL 301
              :| :
Db        301 VKTI 304
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RESULT 5
O1F1_HUMAN
ID   O1F1_HUMAN      STANDARD;      PRT;   312 AA.
AC   O43749; O15246;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Olfactory receptor 1F1 (Olfactory receptor 16-35) (OR16-35).
GN   OR1F1 OR OLFMF.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97434208; PubMed=9288094;
RA   Bernot A., Clepet C., Dasilva C., Devaud C., Petit J.-L.,
RA   Caloustian C., Cruaud C., Samson D., Pulcini F., Weissenbach J.,
RA   Heilig R., Notanicola C., Domingo C., Rozenbaum M., Benchetrit E.,
RA   Topaloglu R., Dewalle M., Dross C., Hadjari P., Dupont M.,
RA   Demaille J.G., Touitou I., Smaoui N., Nedelec B., Mery J.-P.,
RA   Chaabouni H., Delpech M., Grateau G.;
RT   "A candidate gene for familial Mediterranean fever.";
RL   Nat. Genet. 17:25-31(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Bernot A., Heilig R., Clepet C., Smaoui N., Delpech M., da Silva C.,
RA   Devaud C., Petit J.-L., Chiannilkulchai N., Fizames C., Samson D.,
RA   Cruaud C., Caloustian C., Gyapay G., Weissenbach J.;
RT   "A transcriptional map of the FMF region.";
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE OF 68-283 FROM N.A.
RX   MEDLINE=98160182; PubMed=9500546;
RA   Rouquier S.P., Taviaux S., Trask B.J., Brand-Arpon V.,
RA   Van den Engh G., Demaille J.G., Giorgi D.;
RT   "Distribution of olfactory receptor genes in the human genome.";
RL   Nat. Genet. 18:243-250(1998).
RN   [4]
RP   SEQUENCE OF 68-283 FROM N.A.
RA   Fuchs T., Malecova B., Linhart C., Sharan R., Khen M., Herwig R.,
RA   Shmulevich D., Elkon R., Steinfath M., O'Brien J.K., Radelof U.,
RA   Lehrach H., Olender Z., Gluesman G., Lancet D., Shamir R.;
RT   "DEFOG: a practical scheme for deciphering families of genes.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Y14442; CAA74794.1; -.
DR   EMBL; AJ003147; CAA05903.1; -.
DR   EMBL; U86234; AAC39614.1; -.
DR   EMBL; AF399559; AAK95044.1; -.
DR   Genew; HGNC:8194; OR1F1.
DR   MIM; 603232; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Olfaction.
FT   DOMAIN        1     25       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     26     49       1 (POTENTIAL).
FT   DOMAIN       50     57       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     58     79       2 (POTENTIAL).
FT   DOMAIN       80    100       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    101    120       3 (POTENTIAL).
FT   DOMAIN      121    139       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    140    158       4 (POTENTIAL).
FT   DOMAIN      159    196       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    197    219       5 (POTENTIAL).
FT   DOMAIN      220    236       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    237    259       6 (POTENTIAL).
FT   DOMAIN      260    272       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    273    292       7 (POTENTIAL).
FT   DOMAIN      293    312       CYTOPLASMIC (POTENTIAL).
FT   DISULFID     97    189       BY SIMILARITY.
FT   CARBOHYD      5      5       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    191    191       D -> N (IN REF. 1).
FT   CONFLICT    305    305       V -> I (IN REF. 1).
SQ   SEQUENCE   312 AA;  34866 MW;  5C1E1708A18B10E4 CRC64;

  Query Match             43.6%;  Score 702.5;  DB 1;  Length 312;
  Best Local Similarity   44.8%;  Pred. No. 6.1e-46;
  Matches  139;  Conservative   63;  Mismatches  105;  Indels    3;  Gaps    2;

Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              |   ||: |:||: |||:     : | |: | ::|: |: ||:|||::       ||||||
Db          1 MSGTNQSSVSEFLLLGLSRQPQQQHLLFVFFLSMYLATVLGNLLIILSVSIDSCLHTPMY 60

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
              ||||||||:||| |  ||||||   :|| :|||  |:||::|: :|   : ||| ::||
Db         61 FFLSNLSFVDICFSFTTVPKMLANHILETQTISFCGCLTQMYFVFMFVDMDNFLLAVMAY 120

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
              | :||:| ||||   |  ::|  ||  ||:   :: |  | |   | :|  | |  :|||
Db        121 DHFVAVCHPLHYTAKMTHQLCALLVAGLWVVANLNVLLHTLLMAPLSFCADNAITHFFCD 180

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVS-LRKHSAEGRQKALST 239
              |  ::||:|:||:|  ::|::    : :: || :: ||| |  : |:  | :|| || ||
Db        181 VTPLLKLSCSDTHLNEVIILSEGALVMITPFLCILASYMHITCTVLKVPSTKGRWKAFST 240

Qy        240 CSAHFMVVALFFGPCIFIYTRPDTSFSIDK--VVSVFYTVVTPLLNPFIYTLRNEEVKSA 297
              | :|  || ||:   | :|  | :| | :|  : :| |||||:||||||:|||  :| |
Db        241 CGSHLAVVLLFYSTIIAVYFNPLSSHSAEKDTMATVLYTVVTPMLNPFIYSLRNRYLKGA 300

Qy        298 MKQLRQRQVF 307
              :|::  | ||
Db        301 LKKVVGRVVF 310


RESULT 6
O5I1_HUMAN
ID   O5I1_HUMAN      STANDARD;      PRT;   314 AA.
AC   Q13606;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Olfactory receptor 5I1 (Olfactory receptor-like protein OLF1).
GN   OR5I1 OR OLF1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Issel-Tarver L., Rine J.;
RL   Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U56420; AAB01214.1; -.
DR   Genew; HGNC:8347; OR5I1.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Olfaction.
FT   DOMAIN        1     28       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     29     51       1 (POTENTIAL).
FT   DOMAIN       52     59       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     60     81       2 (POTENTIAL).
FT   DOMAIN       82    102       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    103    122       3 (POTENTIAL).
FT   DOMAIN      123    141       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    142    166       4 (POTENTIAL).
FT   DOMAIN      167    207       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    208    228       5 (POTENTIAL).
FT   DOMAIN      229    241       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    242    262       6 (POTENTIAL).
FT   DOMAIN      263    273       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    274    294       7 (POTENTIAL).
FT   DOMAIN      295    314       CYTOPLASMIC (POTENTIAL).
FT   DISULFID     99    191       BY SIMILARITY.
FT   CARBOHYD      7      7       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   314 AA;  36048 MW;  334BE9BF3D9A4D63 CRC64;

  Query Match           43.1%;  Score 694.5;  DB 1;  Length 314;
  Best Local Similarity   43.9%;  Pred. No. 2.4e-45;
  Matches  134;  Conservative   62;  Mismatches  106;  Indels    3;  Gaps    2;

Qy          5 NQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMYFFLS 64
              | | ||||: ||       |::: |: |  :| : | ||| :::     | | ||||||||
Db          7 NYTLVTEFILLGFPTRPELQIVLFLMFLTLYAIILIGNIGLMLLIRIDPHLQTPMYFFLS 66

Qy         65 NLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAYDRYV 124
              ||||:|:|: |  |||||    | | |:||:  |  | :|   ||  | |:|  :||||||
Db         67 NLSFVDLCYFSDIVPKMLVNFLSENKSISYYGCALQFYFFCTFADTESFILAAMAYDRYV 126

Qy        125 AICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCDVPLV 184
              ||| || |  ||:  :|::|:   :||| : ||  |      | ||  |:|: :|||:| :
Db        127 AICNPLLYTVVMSRGICMRLIVLSYLGGNMSSLVHTSFAFILKYCDKNVINHFFCDLPPL 186

Qy        185 IKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRK-HSAEGRQKALSTCSAH 243
              :||:|||| :   |: |   :: : ||: :: ||  ||:|: |  | ||:|  |||::|
Db        187 LKLSCTDTTINEWLLSTYGSSVEIICFIIIIISYFFILLSVLKIRSFSGRKKTFSTCASH 246

Qy        244 FMVVALFFGPCIFIYTRPDTSFS--IDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQL 301
              | :: |  :|||:||   :|   ||::|||||:  |:||| ||:|||::||.| :::
Db        247 LTSVTIYQGTLLFIYSRPSYLYSPNTDKIISVFYTIFIPVLNPLIYSLRNKDVKDAAEKV 306

Qy        302 RQRQV 306
              : :|
Db        307 LRSKV 311


RESULT 7
OLF1_CANFA
ID   OLF1_CANFA     STANDARD;      PRT;   311 AA.
AC   Q95154;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   Olfactory receptor-like protein OLF1.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97008103; PubMed=8855279;
RA   Issel-Tarver L., Rine J.;
RT   "Organization and expression of canine olfactory receptor genes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 93:10897-10902(1996).
CC   -!- FUNCTION: PUTATIVE ODORANT OR SPERM CELL RECEPTOR.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U53679; AAB37239.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Olfaction.
FT   DOMAIN        1     24       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     25     48       1 (POTENTIAL).
FT   DOMAIN       49     56       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     57     78       2 (POTENTIAL).
FT   DOMAIN       79     99       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    100    119       3 (POTENTIAL).
FT   DOMAIN      120    138       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    139    157       4 (POTENTIAL).
FT   DOMAIN      158    195       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    196    218       5 (POTENTIAL).
FT   DOMAIN      219    235       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    236    259       6 (POTENTIAL).
FT   DOMAIN      260    271       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    272    291       7 (POTENTIAL).
FT   DOMAIN      292    311       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD      4      4       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   311 AA;  35209 MW;  05A2132474F543A1 CRC64;

  Query Match           43.0%;  Score 693;  DB 1;  Length 311;
  Best Local Similarity   45.5%;  Pred. No. 3.1e-45;
  Matches  138;  Conservative   56;  Mismatches  105;  Indels    4;  Gaps    3;

Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAPSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              ||  | | ||||: ||       |::: |: |  :| : |:||| :::     | | ||||
Db          1 MDG-NYTLVTEFILLGFPTRPELQIVLFLVFLTLYGIILTGNIGLMMLIRTDPHLQTPMY 59

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
              |||||||| |:| ||  |||||   | | |:||   |  | :|   ||  | |:|  :||
Db         60 FFLSNLSFADLCFSSAIVPKMLVNFLSENKSISLYGCALQFYFSCAFADTESFILAAMAY 119

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
              |||||||  || |  ||:  :|: |:   ::|| : ||  |      | ||  |:|: :|||
Db        120 DRYVAICNPLLYTVVMSRGICVWLIVLSYIGGNMSSLVHTSFAFILKYCDKNVINHFFCD 179

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVS-LRKHSAEGRQKALST 239
              :| ::||:|||| :   |: |   :: : ||: :| ||  || | ||  |: ||:|  ||
Db        180 LPPLLKLSCTDTSVNEWLLSTYGSSVEIFCFIVIVISYYFILRSVLRIRSSSGRKKTFST 239

Qy        240 CSAHFMVVALFFGPCIFIYTRPDTSF--SIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSA 297
              |::|   ||:: |  :|||:||   :  : ||::|||||:: |:||| ||:|||::|| |
Db        240 CASHLTSVAIYQGTLLFIYSRPTYLYTPNTDKIISVFYTIIIPVLNPLIYSLRNKDVKDA 299

Qy        298 MKQ 300
              |:
Db        300 AKR 302
```

```
RESULT 8
OCD2_HUMAN
ID   OCD2_HUMAN     STANDARD;      PRT;   307 AA.
AC   P58182;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Olfactory receptor 12D2 (Hs6M1-20).
GN   OR12D2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Janer M.M., Guillaudeux T., Vu Q., Kutyavin T., Harter H.,
RA   Geraghty D.E.;
RT   "Large scale sequence analysis of the human MHC class I region.";
RL   Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Whitaker H.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AC004171; -; NOT_ANNOTATED_CDS.
DR   EMBL; AL035542; CAB44510.1; -.
DR   Genew; HGNC:8178; OR12D2.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Olfaction.
FT   DOMAIN        1     23       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     24     47       1 (POTENTIAL).
FT   DOMAIN       48     55       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     56     77       2 (POTENTIAL).
FT   DOMAIN       78     98       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     99    118       3 (POTENTIAL).
FT   DOMAIN      119    137       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    138    156       4 (POTENTIAL).
FT   DOMAIN      157    193       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    194    217       5 (POTENTIAL).
FT   DOMAIN      218    235       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    236    258       6 (POTENTIAL).
FT   DOMAIN      259    271       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    272    291       7 (POTENTIAL).
FT   DOMAIN      292    307       CYTOPLASMIC (POTENTIAL).
FT   DISULFID     95    187       BY SIMILARITY.
FT   CARBOHYD      3      3       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   307 AA;  34872 MW;  76DDAC6C2F75C530 CRC64;

  Query Match             42.8%;  Score 689;  DB 1;  Length 307;
  Best Local Similarity   43.9%;  Pred. No. 6.1e-45;
  Matches  134;  Conservative   62;  Mismatches  105;  Indels    4;  Gaps    2;

Qy          4 LNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMYFFL 63
              || | ||||: ||:|| : |:   |: |  || ::::||  :::  :  | ||: |||||
Db          2 LNTTSVTEFLLLGVTDIQELQPPLFVVFLTIYFISVTGNGAVLMIVISDPRLHSLMYFFL 61

Qy         64 SNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAYDRY 123
              |||::|||:|:||:||||:  |   | |||  ||:|| | |      |  |  ::|:|
Db         62 GNLSYLDICYSTVTLPKMLQNFLSTHKAISFLGCISQLHFFHFLGSTESMLFAVMAFDLS 121

Qy        124 VAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCDVPL 183
              |||| || |  :|| ::| |:   :|: |  |:|  : :| || :|| | |  : ||:
Db        122 VAICKPLRYTVIMNPQLCTQMAITIWVIGFFHALLHSVMTSRLNFCGSNRIHHFLCDIKP 181

Qy        184 VIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSL--RKHSAEGRQKALSTCS 241
              ::|||| :| |   |: | :|||::  |   : ||  |:  |  :  |      ||||||:
Db        182 LLKLACGNTELNQWLLSTVTGTIAMGPFFLTLLSYFYIITYLFFKTRSCSMLCKALSTCA 241

Qy        242 AHFMVVALFFGPCIFIYTRP--DTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMK 299
              :|||||  ||: | :| |  |  ::    |::|:: ||||||:||| ||||||:||| |:
Db        242 SHFMVVILFYAPVLFTYIHPALESFMDQDRIVAIMYTVVTPVLNPLIYTLRNKEVKGALG 301

Qy        300 QLRQR 304
              :: :|
Db        302 RVIRR 306


RESULT 9
O2D2_HUMAN
ID   O2D2_HUMAN     STANDARD;      PRT;   308 AA.
AC   Q9H2I0; O95224;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Olfactory receptor 2D2 (Olfactory receptor 11-610) (OR11-610) (HB2).
GN   OR2D2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21310002; PubMed=11416212;
RA   Lane R.P., Cutforth T., Young J., Athanasiou M., Friedman C.,
RA   Rowen L., Evans G., Axel R., Hood L., Trask B.J.;
RT   "Genomic analysis of orthologous mouse and human olfactory receptor
RT   loci.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:7390-7395(2001).
RN   [2]
RP   SEQUENCE OF 67-283 FROM N.A.
RX   MEDLINE=99005533; PubMed=9787077;
RA   Buettner J.A., Glusman G., Ben-Arie N., Ramos P., Lancet D.,
RA   Evans G.A.;
RT   "Organization and evolution of olfactory receptor genes on human
RT   chromosome 11.";
RL   Genomics 53:56-68(1998).
CC   -!- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF321237; AAG45204.1; -.
DR   EMBL; AF065876; AAC70020.1; -.
DR   Genew; HGNC:8244; OR2D2.
DR   GO; GO:0016021; C:integral to membrane; NAS.
DR   GO; GO:0004984; F:olfactory receptor activity; NAS.
DR   GO; GO:0007608; P:olfaction; NAS.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
```

```
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Olfaction.
FT   DOMAIN        1     25       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     26     49       1 (POTENTIAL).
FT   DOMAIN       50     57       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     58     79       2 (POTENTIAL).
FT   DOMAIN       80    100       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    101    120       3 (POTENTIAL).
FT   DOMAIN      121    139       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    140    158       4 (POTENTIAL).
FT   DOMAIN      159    195       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    196    219       5 (POTENTIAL).
FT   DOMAIN      220    236       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    237    259       6 (POTENTIAL).
FT   DOMAIN      260    270       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    271    290       7 (POTENTIAL).
FT   DOMAIN      291    308       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD      5      5       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    134    134       D -> N (IN REF. 1).
SQ   SEQUENCE   308 AA;  34130 MW;  0651A5973426082A CRC64;

  Query Match             42.6%;  Score 686.5;  DB 1;  Length 308;
  Best Local Similarity   43.4%;  Pred. No. 9.5e-45;
  Matches  135;  Conservative   58;  Mismatches  105;  Indels   13;  Gaps    2;

Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              |  :|||:||||: |||:|    | | |:    :|::|: ||:|:|        ||||||
Db          1 MRQINQTQVTEFLLLGLSDGPHTEQLLFIVLLGVYLVTVLGNLLLISLVHVDSQLHTPMY 60

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
              ||| |||  |:| |:  ||:| |  ||  :| |:|  |  :| |  :| | :  || :::|
Db         61 FFLCNLSLADLCFSTNIVPQALVHLLSRKKVIAFTLCAARLLFFLIFGCTQCALLAVMSY 120

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
              ||||||| || ||::|  :||:||    |  | : |:  |  |:|||| | | |  :||:
Db        121 DRYVAICNPLRYPDIMTWKVCVQLATGSWTSGILVSVVDTTFTLRLPYRGSNSIAHFFCE 180

Qy        181 VPLVIKLACTDT-------YLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGR 233
              | :: || ||| :|||::|    : :  || :|:  :|:  ::  |  |
Db        181 APALLILASTDTHASEMAIFLTGVVI------LLIPVFLILVSYGRIIVTVVKMKSTVGS 234

Qy        234 QKALSTCSAHFMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEE 293
              || ||| :| ||| ||:|  |  |  | :|   :| ||||| :|||:||| ||:|||::
Db        235 LKAFSTCGSHLMVVILFYGSAIITYMTPKSSKQQEKSVSVFYAIVTPMLNPLIYSLRNKD 294

Qy        294 VKSAMKQLRQR 304
              ||:|:::: |
Db        295 VKAALRKVATR 305


RESULT 10
OLF5_RAT
ID   OLF5_RAT       STANDARD;      PRT;   313 AA.
AC   P23266;
DT   01-NOV-1991 (Rel. 20, Created)
DT   01-NOV-1991 (Rel. 20, Last sequence update)
DT   01-JUL-1993 (Rel. 26, Last annotation update)
DE   Olfactory receptor-like protein F5.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91191556; PubMed=1840504;
RA   Buck L., Axel R.;
RT   "A novel multigene family may encode odorant receptors: a molecular
RT   basis for odor recognition.";
RL   Cell 65:175-187(1991).
CC   -!- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: OLFACTORY EPITHELIUM.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M64377; AAA41740.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Olfaction.
FT   DOMAIN        1     25       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     26     50       1 (POTENTIAL).
FT   DOMAIN       51     57       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     58     79       2 (POTENTIAL).
FT   DOMAIN       80    100       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    101    120       3 (POTENTIAL).
FT   DOMAIN      121    139       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    140    158       4 (POTENTIAL).
FT   DOMAIN      159    196       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    197    219       5 (POTENTIAL).
FT   DOMAIN      220    236       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    237    260       6 (POTENTIAL).
FT   DOMAIN      261    272       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    273    292       7 (POTENTIAL).
FT   DOMAIN      293    313       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD      5      5       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID     97    189       BY SIMILARITY.
SQ   SEQUENCE   313 AA;  34703 MW;  2FD7BCD6E36D8815 CRC64;

  Query Match             42.6%;  Score 686.5;  DB 1;  Length 313;
  Best Local Similarity   43.8%;  Pred. No. 9.6e-45;
  Matches  133;  Conservative   63;  Mismatches  105;  Indels    3;  Gaps    2;

Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              | | ||: ||||: |||:     : | |: |  :|: |: ||:|||:|      ||||||
Db          1 MSSTNQSSVTEFLLLGLSRQPQQQQLLFLLFLIMYLATVLGNLLIILAIGTDSRLHTPMY 60

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
              ||||||||:|:| || ||||:|   :|  : |||  |:|||:|| :|   : ||| :::|
Db         61 FFLSNLSFVDVCFSSTTVPKVLANHILGSQAISFSGCLTQLYFLAVFGNMDNFLLAVMSY 120

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
              ||:|||| ||||   |  ::|: ||   |:   :: |    |  || :|  |:|  :|||
Db        121 DRFVAICHPLHYTTKMTRQLCVLLVVGSWVVANMNCLLHILLMARLSFCADNMIPHFFCD 180

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVS-LRKHSAEGRQKALST 239
                ::||:|:||:|  ::|:|    : :: |: :: ||: |  : ||  |  |  |: ||
Db        181 GTPLLKLSCSDTHLNELMILTEGAVVMVTPFVCILISYIHITCAVLRVSSPRGGWKSFST 240

Qy        240 CSAHFMVVALFFGPCIFIYTRPDTSF--SIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSA 297
              | :|  || ||:|  | :|  | :|      |   :| | ||||:|||||:||| ::|:|
Db        241 CGSHLAVVCLFYGTVIAVYFNPSSSHLAGRDMAAAVMYAVVTPMLNPFIYSLRNSDMKAA 300

Qy        298 MKQL 301
              ::::
Db        301 LRKV 304


RESULT 11
OAC1_HUMAN
ID   OAC1_HUMAN     STANDARD;      PRT;   312 AA.
AC   Q96KK4;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Olfactory receptor 10C1 (Hs6M1-17).
```

```
GN   OR10C1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Whitaker H.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AL035542; CAB44507.1; ALT_INIT.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Olfaction.
FT   DOMAIN        1     24       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     25     48       1 (POTENTIAL).
FT   DOMAIN       49     56       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     57     78       2 (POTENTIAL).
FT   DOMAIN       79     99       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    100    119       3 (POTENTIAL).
FT   DOMAIN      120    138       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    139    157       4 (POTENTIAL).
FT   DOMAIN      158    194       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    195    218       5 (POTENTIAL).
FT   DOMAIN      219    235       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    236    258       6 (POTENTIAL).
FT   DOMAIN      259    271       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    272    291       7 (POTENTIAL).
FT   DOMAIN      292    312       CYTOPLASMIC (POTENTIAL).
FT   DISULFID     96    188       BY SIMILARITY.
FT   CARBOHYD      4      4       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   312 AA;  34351 MW;  B6FD6E0E700CB2CC CRC64;

  Query Match             42.3%;  Score 681.5;  DB 1;  Length 312;
  Best Local Similarity   45.6%;  Pred. No. 2.3e-44;
  Matches  140;  Conservative   55;  Mismatches  109;  Indels    3;  Gaps    2;

Qy          3 SLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMYFF 62
              | | : ||||: || :    |: | |  |  ||:||::|| ||::      :| :|||||
Db          2 SANTSMVTEFLLLGFSHLADLQGLLFSVFLTIYLLTVAGNFLIVVLVSTDAALQSPMYFF 61

Qy         63 LSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAYDR 122
              |  || ::| ::||||| :|  ||  |: ||   |  |:||   |   |  ||  :||||
Db         62 LRTLSALEIGYTSVTVPLLLHHLLTGRRHISRSGCALQMFFFLFFGATECCLLAAMAYDR 121

Qy        123 YVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCDVP 182
              | ||| || || ::: |||:||  : |  | :  || |     ||:|||| |  :||::
Db        122 YAAICEPLRYPLLLSHRVCLQLAGSAWACGVLVGLGHTPFIFSLPFCGPNTIPQFFCEIQ 181

Qy        183 LVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSL-RKHSAEGRQKALSTCS 241
                |::| | || |  : |:  :  : | |  :: ||  |||:: |  |  ||:|| ||||
Db        182 PVLQLVCGDTSLNELQIILATALLILCPFGLILGSYGRILVTIFRIPSVAGRRKAFSTCS 241

Qy        242 AHFMVVALFFGPCIFIYTRPDTSF--SIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMK 299
              :| :||:||:|  :||| ||  |:  : | :||:|| ||||:||| ||:||| |||:|:|
Db        242 SHLIVVSLFYGTALFIYIRPKASYDPATDPLVSLFYAVVTPILNPIIYSLRNTEVKAALK 301

Qy        300 QLRQRQV 306
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              :  |: |
Db        302 RTIQKTV 308


RESULT 12
OCD3_HUMAN
ID   OCD3_HUMAN     STANDARD;      PRT;   316 AA.
AC   Q9UGF7;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Olfactory receptor 12D3 (Hs6M1-27).
GN   OR12D3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RA   Volz A., Ehlers A., Younger R., Forbes S., Trowsdale J., Beck S.,
RA   Ziegler A.;
RT   "Complex transcriptional control of MHC-linked olfactory receptor
RT   genes includes long distance and extensive alternative splicing, exon
RT   sharing and premature polyadenylation.";
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Tracey A.;
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ459858; CAD31041.1; -.
DR   EMBL; AL096770; CAB65796.1; -.
DR   Genew; HGNC:13963; OR12D3.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Olfaction.
FT   DOMAIN        1     23       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     24     47       1 (POTENTIAL).
FT   DOMAIN       48     55       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     56     77       2 (POTENTIAL).
FT   DOMAIN       78     98       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     99    118       3 (POTENTIAL).
FT   DOMAIN      119    137       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    138    156       4 (POTENTIAL).
FT   DOMAIN      157    193       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    194    219       5 (POTENTIAL).
FT   DOMAIN      220    235       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    236    258       6 (POTENTIAL).
FT   DOMAIN      259    271       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    272    291       7 (POTENTIAL).
FT   DOMAIN      292    316       CYTOPLASMIC (POTENTIAL).
FT   DISULFID     95    187       BY SIMILARITY.
FT   CARBOHYD      3      3       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   316 AA;  35791 MW;  07FDCF869D8989B2 CRC64;

  Query Match             42.3%;  Score 681;  DB 1;  Length 316;
  Best Local Similarity   44.6%;  Pred. No. 2.5e-44;
```

```
  Matches  137;  Conservative   60;  Mismatches  106;  Indels    4;  Gaps    2;

Qy          5 NQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMYFFLS 64
              | | : ||: |||| : |:  ||  |  ||:: | ||  |::  || | ||:||||||
Db          3 NVTTMNEFLLLGLTGVQELQPFFFGIFLIIYLINLIGNGSILVMVVLEPQLHSPMYFFLG 62

Qy         65 NLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAYDRYV 124
              ||| :|| :|||:||:|  |:  |: ||| ||||| | |      | || |:|:||:|
Db         63 NLSCLDISYSSVTLPKLLVNLVCSRRAISFLGCITQLHFFHFLGSTEAILLAIMAFDRFV 122

Qy        125 AICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCDVPLV 184
              ||| || |  :|| :||| |  | ||    ::|  : :|  | :||   :: :| ||  :
Db        123 AICNPLRYTVIMNPQVCILLAAAAWLISFFYALMHSVMTAHLSFCGSQKLNHFFYDVKPL 182

Qy        185 IKLACTDTYLTGILIVTNSGTISLSCFLAVVTS--YMVILVSLRKHSAEGRQKALSTCSA 242
              ::|||:|| |   |:   :|:||:  |   : |  |::  :  :  |      ||||||::
Db        183 LELACSDTLLNQWLLSIVTGSISMGAFFLTLLSCFYVIGFLLFKNRSCRILHKALSTCAS 242

Qy        243 HFMVVALFFGPCIFIYTRPDTSFSI--DKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300
              ||||| ||:||  | | || :: |:  |:::: |: |||:||| ||||||:||  |:|:
Db        243 HFMVVCLFYGPVGFTYIRPASATSMIQDRIMAIMYSAVTPVLNPLIYTLRNKEVMMALKK 302

Qy        301 LRQRQVF 307
              :  |::|
Db        303 IFGRKLF 309


RESULT 13
O5BG_HUMAN
ID   O5BG_HUMAN     STANDARD;      PRT;   314 AA.
AC   Q96R08;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Olfactory receptor 5B16.
GN   OR5B16.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE OF 66-281 FROM N.A.
RA   Fuchs T., Malecova B., Linhart C., Sharan R., Khen M., Herwig R.,
RA   Shmulevich D., Elkon R., Steinfath M., O'Brien J.K., Radelof U.,
RA   Lehrach H., Olender Z., Gluesman G., Lancet D., Shamir R.;
RT   "DEFOG: a practical scheme for deciphering families of genes.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF399637; AAK95122.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Olfaction.
FT   DOMAIN       1     23       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     24    47       1 (POTENTIAL).
FT   DOMAIN       48    55       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     56    77       2 (POTENTIAL).
FT   DOMAIN       78    98       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     99    118      3 (POTENTIAL).
FT   DOMAIN       119   137      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     138   156      4 (POTENTIAL).
FT   DOMAIN       157   193      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     194   217      5 (POTENTIAL).
FT   DOMAIN       218   234      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     235   257      6 (POTENTIAL).
FT   DOMAIN       258   270      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     271   290      7 (POTENTIAL).
FT   DOMAIN       291   314      CYTOPLASMIC (POTENTIAL).
FT   DISULFID     95    187      BY SIMILARITY.
FT   CARBOHYD     3     3        N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     261   261      N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   314 AA;  35181 MW;  93BB84F1CACA68F1 CRC64;

  Query Match             42.1%;  Score 677.5;  DB 1;  Length 314;
  Best Local Similarity   44.1%;  Pred. No. 4.6e-44;
  Matches  132;  Conservative   58;  Mismatches  106;  Indels    3;  Gaps    2;

Qy          5 NQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMYFFLS 64
              | | |||| : ||||:  |::  |: |  ||::|| ||: :|   :    ||||||||||
Db          3 NNTEVTEFILVGLTDDPELQIPLFIVFLFIYLITLVGNLGMIELILLDSCLHTPMYFFLS 62

Qy         65 NLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAYDRYV 124
              ||| :|  :||   ||:: | |   | | :: | || ||   |  || |||  :|||||
Db         63 NLSLVDFGYSSAVTPKVMVGFLTGDKFILYNACATQFFFFVAFITAESFLLASMAYDRYA 122

Qy        125 AICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCDVPLV 184
              |:| ||||   |  ||  |    :: | :::   |  | || :|  |::: :||| | :
Db        123 ALCKPLHYTTTMTTNVCACLAIGSYICGFLNASIHTGNTFRLSFCRSNVVEHFFCDAPPL 182

Qy        185 IKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRK-HSAEGRQKALSTCSAH 243
              : |:|:| |:: ::|    |   |   | :: ||: | ::: |  | |||||| |||::|
Db        183 LTLSCSDNYISEMVIPFVVGFNDLFSILVILISYLFIFITIMKMRSPEGRQKAFSTCASH 242

Qy        244 FMVVALFFGPCIFIYTRPDTS--FSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300
              |::|:|  ||:| ||::|    ||: |||| :| |:||| :|:|||:|||| |:
Db        243 LTAVSIFYGTGIFMYLRPNSSHFMGTDKMASVFYAIVIPMLNPLVYSLRNKEVKSAFKK 301


RESULT 14
O7C1_HUMAN
ID   O7C1_HUMAN     STANDARD;      PRT;   320 AA.
AC   O76099; Q15621;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Olfactory receptor 7C1 (Olfactory receptor TPCR86).
GN   OR7C1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Sperm;
RA   Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,
RA   Burkhart-Schultz K.J., Gordon L., Kyle A., Ramirez M., Stilwagen S.,
RA   Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,
RA   Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
RA   Liu S., Attix C., Andreise T., Trankheim M., Amico-Keller G.,
RA   Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
RA   Kronmiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,
RA   Kobayashi A., Olsen A.S., Carrano A.V.;
RT   "Sequence analysis of an ~1.5 Mb olfactory receptor (OLFR) cluster in
RT   19q13.1.";
RL   Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 126-282 FROM N.A.
RC   TISSUE=Testis;
RX   MEDLINE=97224452; PubMed=9119360;
RA   Vanderhaeghen P., Schurmans S., Vassart G., Parmentier M.;
RT   "Specific repertoire of olfactory receptor genes in the male germ
RT   cells of several mammalian species.";
RL   Genomics 39:239-246(1997).
```

```
CC   -!- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AC005255; AAC25625.1; -.
DR   EMBL; X89676; CAA61823.1; -.
DR   PIR; S58004; S58004.
DR   Genew; HGNC:8373; OR7C1.
DR   GO; GO:0007582; P:physiological processes; TAS.
DR   GO; GO:0007283; P:spermatogenesis; TAS.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Olfaction.
FT   DOMAIN       1     25       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     26    49       1 (POTENTIAL).
FT   DOMAIN       50    57       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     58    79       2 (POTENTIAL).
FT   DOMAIN       80    100      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     101   120      3 (POTENTIAL).
FT   DOMAIN       121   139      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     140   158      4 (POTENTIAL).
FT   DOMAIN       159   196      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     197   219      5 (POTENTIAL).
FT   DOMAIN       220   236      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     237   259      6 (POTENTIAL).
FT   DOMAIN       260   272      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     273   292      7 (POTENTIAL).
FT   DOMAIN       293   313      CYTOPLASMIC (POTENTIAL).
FT   DISULFID     97    189      BY SIMILARITY.
FT   CARBOHYD     5     5        N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     171   171      E -> K (IN REF. 2).
FT   CONFLICT     210   210      S -> P (IN REF. 2).
FT   CONFLICT     247   247      V -> L (IN REF. 2).
SQ   SEQUENCE   320 AA;  35518 MW;  BBDCC409721D70C4 CRC64;

  Query Match             42.0%;  Score 676.5;  DB 1;  Length 320;
  Best Local Similarity   42.1%;  Pred. No. 5.5e-44;
  Matches  134;  Conservative   64;  Mismatches  113;  Indels    7;  Gaps    3;

Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              |:: |||   ||: || :    :: : |  | ::|::| :||:|||:|      ||||||
Db          1 METGNQTHAQEFLLLGFSATSEIQFILFGLFLSMYLVTFTGNLLIILAICSDSHLHTPMY 60

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
              |||||||| |:| :| ||||||  :| : | |::  |::|:||   | | :  || ::||
Db         61 FFLSNLSFADLCFTSTTVPKMLLNILTQNKFITYAGCLSQIFFFTSFGCLDNLLLTVMAY 120

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
              ||:||:| |||| :|| ::|  ||    |    : || :|   :|| :|    |  :|||
Db        121 DRFVAVCHPLHYTVIMNPQLCGLLVLGSWCISVMGSLLETLTVLRLSFCTEMEIPHFFCD 180

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQ-KALST 239
              :  |:||||:||::  ::|   :| : :  |  :  ||  |: |: : |: ||: || ||
Db        181 LLEVLKLACSDTFINNVVIYFATGVLGVISFTGIFFSYYKIVFSILRISSAGRKHKAFST 240

Qy        240 CSAHFMVVALFFGPCIFIY----TRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVK 295
              | :|  || ||:|    :|      | :  |:  | || ||:|||:||||||:||| ::|
Db        241 CGSHLSVVTLFYGTGFGVYLSSAATPSSRTSL--VASVMYTMVTPMLNPFIYSLRNTDMK 298

Qy        296 SAMKQLRQRQVFFTKSYT 313
                |: :|  |  ||   |
```

```
Db        299 RALGRLLSRATFFNGDIT 316


RESULT 15
O1Q1_HUMAN
ID   O1Q1_HUMAN     STANDARD;      PRT;   314 AA.
AC   Q15612;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Olfactory receptor 1Q1 (Olfactory receptor TPCR106) (Olfactory
DE   receptor 9-A) (OR9-A).
GN   OR1Q1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE OF 126-282 FROM N.A.
RC   TISSUE=Testis;
RX   MEDLINE=97224452; PubMed=9119360;
RA   Vanderhaeghen P., Schurmans S., Vassart G., Parmentier M.;
RT   "Specific repertoire of olfactory receptor genes in the male germ
RT   cells of several mammalian species.";
RL   Genomics 39:239-246(1997).
CC   -!- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X89667; CAA61814.1; -.
DR   PIR; S58012; S58012.
DR   Genew; HGNC:8223; OR1Q1.
DR   GO; GO:0016021; C:integral to membrane; NAS.
DR   GO; GO:0004984; F:olfactory receptor activity; NAS.
DR   GO; GO:0007608; P:olfaction; NAS.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Multigene family; Olfaction.
FT   DOMAIN       1     25       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     26    49       1 (POTENTIAL).
FT   DOMAIN       50    57       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     58    79       2 (POTENTIAL).
FT   DOMAIN       80    100      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     101   120      3 (POTENTIAL).
FT   DOMAIN       121   139      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     140   158      4 (POTENTIAL).
FT   DOMAIN       159   195      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     196   219      5 (POTENTIAL).
FT   DOMAIN       220   236      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     237   259      6 (POTENTIAL).
FT   DOMAIN       260   272      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     273   292      7 (POTENTIAL).
FT   DOMAIN       293   314      CYTOPLASMIC (POTENTIAL).
FT   DISULFID     97    189      BY SIMILARITY.
FT   CARBOHYD     5     5        N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     126   126      I -> F (IN REF. 1).
SQ   SEQUENCE   314 AA;  35615 MW;  50D0AB08946B4EFC CRC64;

  Query Match             41.9%;  Score 675;  DB 1;  Length 314;
  Best Local Similarity   43.8%;  Pred. No. 7e-44;
  Matches  137;  Conservative   64;  Mismatches  106;  Indels    6;  Gaps    5;
```

```
Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              ||: | | |: || ||:: :   ::  |: || :| : :|||: ||| :  | || |||
Db          1 MDNSNWTSVSHFVLLGISTHPEEQIPLFLVFSLMYAINISGNLAIITLILSAPRLHIPMY 60

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
               |||||:  ||| :| ||||||: :    | ||:  |: | :|   ||  | |:| ::||
Db         61 IFLSNLALTDICFTSTTVPKMLQIIFSPTKVISYTGCLAQTYFFICFAVMENFILAVMAY 120

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
              |||:||| | ||  ::   :|:::|        :|::  ||| :| :|  | |  :|||
Db        121 DRYIAICHPFHYTMILTRMLCVKMVVMCHALSHLHAMLHTFLMGQLIFCADNRIPHFFCD 180

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVT-SY-MVILVSLRKHSAEGRQKALS 238
              :  ::|::|| ||| ::| |  | : :|  || :| ||  :||| ||  ||:|| |  |
Db        181 LYALMKISCTSTYLNTLMIHT-EGAVVISGALAFITASYACIILVVLRIPSAKGRWKTFS 239

Qy        239 TCSAHFMVVALFFGPCIFIYTRPDTSFSIDK--VVSVFYTVVTPLLNPFIYTLRNEEVKS 296
              || :|  |||:|:|   ::| || :|:|: |  :::| ||||||:|||||:||| :||
Db        240 TCGSHLTVVAIFYGTLSWVYFRPLSSYSVTKGRIITVVYTVVTPMLNPFIYSLRNGDVKG 299

Qy        297 A-MKQLRQRQVFF 308
               || : : | ||
Db        300 GFMKWMSRMQTFF 312
```

Search completed: August 12, 2003, 16:07:15
Job time : 24 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 12, 2003, 16:01:51 ; Search time 39 Seconds
(without alignments)
771.815 Million cell updates/sec

Title: US-09-807-132-4
Perfect score: 1611
Sequence: 1 MDSLNQTRVTEFVFLGLTDN.....VKSAMKQLRQRQVFFTKSYT 313

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	822	51.0	307	2	S29710	olfactory receptor
2	731	45.4	318	2	JC5202	chemoreceptor TB64
3	680.5	42.2	313	2	B23701	olfactory receptor
4	674.5	41.9	333	2	A23701	olfactory receptor
5	661.5	41.1	310	2	E23701	olfactory receptor
6	660	41.0	327	2	F23701	olfactory receptor
7	659.5	40.9	312	2	A46247	olfactory receptor
8	658.5	40.9	314	2	H23701	olfactory receptor
9	657.5	40.8	309	1	S51356	olfactory receptor
10	656	40.7	314	2	S20572	olfactory receptor
11	656	40.7	314	2	A37286	olfactory receptor
12	655	40.7	313	2	S20571	olfactory receptor
13	653.5	40.6	312	2	I23701	olfactory receptor
14	645	40.0	305	2	S29711	olfactory factor O
15	644.5	40.0	311	2	JC5200	chemoreceptor TB33
16	644.5	40.0	314	2	S29707	olfactory receptor
17	644.5	40.0	319	2	JC5624	olfactory receptor
18	643.5	39.9	312	2	S29708	olfactory receptor
19	638.5	39.6	312	2	G23701	olfactory receptor
20	616	38.2	315	2	JC5836	olfactory receptor
21	615.5	38.2	304	2	S29709	olfactory receptor
22	602.5	37.4	315	2	JC4658	olfactory receptor
23	602	37.4	317	2	D23701	olfactory receptor
24	600	37.2	312	2	A48413	probable olfactory
25	593.5	36.8	315	2	JC5201	chemoreceptor TB56
26	586.5	36.4	316	2	A57069	olfactory receptor
27	555	34.5	320	2	S20573	olfactory receptor
28	554.5	34.4	311	2	C23701	olfactory receptor
29	530.5	32.9	312	2	A46750	olfactory receptor
30	471.5	29.3	234	2	S29000	G protein-coupled
31	466.5	29.0	264	2	PC4369	olfactory receptor
32	453	28.1	154	2	S58052	probable olfactory
33	452.5	28.1	321	2	H45774	odorant receptor 3
34	451.5	28.0	222	2	B40745	odorant receptor (
35	451	28.0	143	2	S58071	probable olfactory
36	443	27.5	143	2	S58006	probable olfactory
37	437	27.1	154	2	S58015	probable olfactory
38	436.5	27.1	216	2	I38481	olfactory receptor
39	432.5	26.8	216	2	I38474	olfactory receptor
40	428	26.6	225	2	I38478	olfactory receptor
41	427.5	26.5	222	2	D40745	odorant receptor (
42	426.5	26.5	216	2	I38470	olfactory receptor
43	426.5	26.5	222	2	C40745	odorant receptor (
44	419.5	26.0	232	2	S29001	G protein-coupled
45	419	26.0	328	2	G45774	odorant receptor 2

ALIGNMENTS

RESULT 1
S29710
olfactory receptor OR18 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 04-Sep-1998
C;Accession: S29710
R;Raming, K.; Krieger, J.; Strotmann, J.; Boekhoff, I.; Kubick, S.; Baumstark, C.; Bree
Nature 361, 353-356, 1993
A;Title: Cloning and expression of odorant receptors.
A;Reference number: S29707; MUID:93149273; PMID:7678922
A;Accession: S29710
A;Molecule type: mRNA
A;Residues: 1-307 <RAM>
C;Superfamily: olfactory receptor OR14

Query Match 51.0%; Score 822; DB 2; Length 307;
Best Local Similarity 51.2%; Pred. No. 2.1e-63;
Matches 150; Conservative 55; Mismatches 88; Indels 0; Gaps 0;

```
Qy          9 VTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMYPFLSNLSF 68
              :|||: |||| :       |: |  ||::|: ||:||::  : :||| :||||||::||
Db          7 ITEFILLGLTQDPDGRKALFVIFFLIYIVTMMGNLLIVVTVIASPSLGSPMYFFLASLSL 66

Qy         69 IDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAYDRYVAICT 128
              :|   |:   ||::  || ::|||||  |::|||  |||   :| :|: :|||||||||
Db         67 LDALFSTAISPKLIADLLYDQKTISFRACMSQLFIEHLFGGVDIVILVAMAYDRYVAICK 126

Qy        129 PLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCDVPLVIKLA 188
              ||||  :|| |||| |:   | ||  ||| |       ||:||||:|| : ||:  :: ||
Db        127 PLHYLAIMNRRVCITLLIFAWTGGFTHSLIQIVFVYNLPFCGPNVIDHFICDMSPLLVLA 186

Qy        189 CTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTCSAHFMVVA 248
              |||||  |: :: | |   :  |  :: || :|| ||:  | |||:||||||:| :||
Db        187 CTDTYFIGLTVIANGGVNCIVIFTLLLGSYGIILRSLKTQSQEGRRKALSTCSSHILVVI 246

Qy        249 LFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQL 301
              ||| ||||:| ||  :| ||| ::||||::||:||| |||||| |:|| ||:|
Db        247 LFPVPCIFMYARPVYNFPIDKCITVFYTIITPMLNPLIYTLRNSEIKSCMKKL 299
```

RESULT 2
JC5202
chemoreceptor TB641 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 26-Aug-1999
C;Accession: JC5202; PC4304
R;Thomas, M.B.; Haines, S.L.; Akeson, R.A.
Gene 178, 1-5, 1996
A;Title: Chemoreceptors expressed in taste, olfactory and male reproductive tissues.
A;Reference number: JC5200; MUID:97080538; PMID:8921883
A;Accession: JC5202
A;Status: preliminary; nucleic acid sequence not shown

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A;Molecule type: DNA
A;Residues: 1-318 <THO1>
A;Cross-references: GB:U50949; NID:g1256392; PIDN:AAC52911.1; PID:g1256393
A;Accession: PC4304
A;Status: preliminary
A;Molecule type: protein
A;Residues: 145-153;245-253 <THO2>
A;Experimental source: taste bud
C;Comment: This protein is coupled to a GTP-binding protein-mediated signal transduction
C;Genetics:
A;Gene: tb641
C;Superfamily: olfactory receptor OR14
C;Keywords: olfaction; taste bud; transmembrane protein
F;30-53/Domain: transmembrane #status predicted <TM1>
F;63-84/Domain: transmembrane #status predicted <TM2>
F;106-125/Domain: transmembrane #status predicted <TM3>
F;145-169/Domain: transmembrane #status predicted <TM4>
F;202-224/Domain: transmembrane #status predicted <TM5>
F;243-265/Domain: transmembrane #status predicted <TM6>
F;276-296/Domain: transmembrane #status predicted <TM7>

  Query Match             45.4%;  Score 731;  DB 2;  Length 318;
  Best Local Similarity   46.6%;  Pred. No. 1.5e-55;
  Matches  139;  Conservative   54;  Mismatches  103;  Indels    2;  Gaps    2;

Qy          7 TRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHT-PMYFFLSN 65
              | ||:|: |||      |    |: |  ||:||  ||:||::     | ||  |||  |
Db         11 TVVTDFLLLGLAHPPNLRTFLFLVFLLIYILTQLGNLLILLTVWADPKLHARPMYILLGV 70

Qy         66 LSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAYDRYVA 125
              |||:|:  ||| ||:::       | |:|  |: ||:| |     : ||  ::|||||:|
Db         71 LSFLDMWLSSVIVPRIILNFTPANKAIAFGGCVAQLYFFHFLGSTQCFLYTLMAYDRYLA 130

Qy        126 ICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCDVPLVI 185
              || || || :|| ::|  ||   |: |::|   |  || |||||||  :| :|||:| |:
Db        131 ICQPLRYPVLMNGKLCTILVAGAWVAGSIHGSIQATLTFRLPYCGPKEVDYFFCDIPAVL 190

Qy        186 KLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRK-HSAEGRQKALSTCSAHF 244
              :||| || :  ::   : | :: |||| :: ||  |: :: |  :|:||::| ||| :|
Db        191 RLACADTAINELVTFVDIGVVAASCFLLILLSYANIVHAILKIRTADGRRRAFSTCGSHL 250

Qy        245 MVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQLR 302
               || ::: ||||||  |  :  | |  |:|||||||||||| ||||||:|| ||:|:||
Db        251 TVVTVYYVPCIFIYLRAGSKSSFDGAVAVFYTVVTPLLNPLIYTLRNQEVNSALKRLR 308


RESULT 3
B23701
olfactory receptor F5 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 04-Sep-1998
C;Accession: B23701
R;Buck, L.; Axel, R.
Cell 65, 175-187, 1991
A;Title: A novel multigene family may encode odorant receptors: a molecular basis for od
A;Reference number: A23701; MUID:91191556; PMID:1840504
A;Accession: B23701
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-313 <BUC>
A;Cross-references: GB:M64377
C;Superfamily: olfactory receptor OR14
C;Keywords: G protein-coupled receptor; transmembrane protein

  Query Match             42.2%;  Score 680.5;  DB 2;  Length 313;
  Best Local Similarity   43.4%;  Pred. No. 3.3e-51;
  Matches  132;  Conservative   63;  Mismatches  106;  Indels    3;  Gaps    2;

Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              | | ||: ||||: |||:     : | |: |  :|: |: ||:|||:|      ||||||
Db          1 MSSTNQSSVTEFLLLGLSRQPQQQQLLFLLFLIMYLATVLGNLLIILAIGTDSRLHTPMY 60

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
              ||||||||:|:| || ||||:|   :|  : |||  |:|||:|| :|   : ||| :::|
Db         61 FFLSNLSFVDVCFSSTTVPKVLANHILGSQAISFSGCLTQLYFLAVFGNMDNFLLAVMSY 120

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
              ||:|||| ||||   |  ::|: ||   |:   ::  |     |  |  :|  |:|  :|||
Db        121 DRFVAICHPLHYTTKMTRQLCVLLVVGSWVVANMNCLLHILLMARKSFCADNMIPHFFCD 180

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVS-LRKHSAEGRQKALST 239
                 ::||:|:||:|  ::|:|    : :: |: :: ||: |  : ||  |  |  |: ||
Db        181 GTPLLKLSCSDTHLNELMILTEGAVVMVTPFVCILISYIHITCAVLRVSSPRGGWKSFST 240

Qy        240 CSAHFMVVALFFGPCIFIYTRPDTSF--SIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSA 297
              | :|  || ||:|  | :|  | :|      |   :| | ||||:|||||:||| ::|:|
Db        241 CGSHLAVVCLFYGTVIAVYFNPSSSHLAGRDMAAAVMYAVVTPMLNPFIYSLRNSDMKAA 300

Qy        298 MKQL 301
              ::::
Db        301 LRKV 304


RESULT 4
A23701
olfactory receptor F3 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-Aug-1999
C;Accession: A23701
R;Buck, L.; Axel, R.
Cell 65, 175-187, 1991
A;Title: A novel multigene family may encode odorant receptors: a molecular basis for o
A;Reference number: A23701; MUID:91191556; PMID:1840504
A;Accession: A23701
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-333 <BUC>
A;Cross-references: GB:M64376; NID:g205813; PIDN:AAA41739.1; PID:g205814
C;Superfamily: olfactory receptor OR14
C;Keywords: G protein-coupled receptor; transmembrane protein

  Query Match             41.9%;  Score 674.5;  DB 2;  Length 333;
  Best Local Similarity   43.9%;  Pred. No. 1.1e-50;
  Matches  133;  Conservative   62;  Mismatches  105;  Indels    3;  Gaps    2;

Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              ||| |:|||:||: ||  :|: |: | :  | ::|::|: ||| ||:| :  | ||||||
Db          1 MDSSNRTRVSEFLLLGFVENKDLQPLIYGLFLSMYLVTVIGNISIIVAIISDPCLHTPMY 60

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
              ||||||||:|||  | ||||||  :  :   |::  ||||::|  ||   : ||| |:||
Db         61 FFLSNLSFVDICFISTTVPKMLVNIQTQNNVITYAGCITQIYFFLLFVELDNFLLTIMAY 120

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
              |||||||:|||  :||  ::|  ||    |:   :|:| |: : : ||:|    |  |||:
Db        121 DRYVAICHPMHYTVIMNYKLCGFLVLVSWIVSVLHALFQSLMMLALPFCTHLEIPHYFCE 180

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSL-RKHSAEGRQKALST 239
                ||:| |:| :|  ::|      ::      :  ||  |: |:    |  |: || ||
Db        181 PNQVIQLTCSDAFLNDLVIYFTLVLLATVPLAGIFYSYFKIVSSICAISSVHGKYKAFST 240

Qy        240 CSAHFMVVALFF--GPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSA 297
              |::|  ||:||:  |  ::: :  : |        || ||||||::|||||:|||::|||
Db        241 CASHLSVVSLFYCTGLGVYLSSAANNSSQASATASVMYTVVTPMVNPFIYSLRNKDVKSV 300

Qy        298 MKQ 300
              :|:
Db        301 LKK 303


RESULT 5
E23701
olfactory receptor I3 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-Aug-1999
C;Accession: E23701
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R;Buck, L.; Axel, R.
Cell 65, 175-187, 1991
A;Title: A novel multigene family may encode odorant receptors: a molecular basis for od
A;Reference number: A23701; MUID:91191556; PMID:1840504
A;Accession: E23701
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-310 <BUC>
A;Cross-references: GB:M64385; NID:g205831; PIDN:AAA41748.1; PID:g205832
C;Superfamily: olfactory receptor OR14
C;Keywords: G protein-coupled receptor; transmembrane protein

  Query Match             41.1%;  Score 661.5;  DB 2;  Length 310;
  Best Local Similarity   43.4%;  Pred. No. 1.4e-49;
  Matches  129;  Conservative   64;  Mismatches  101;  Indels    3;  Gaps    2;

Qy          5 NQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMYFFLS 64
              ||| :|:|: |||       : ||:  |  :|: |: ||:|||:        |||||| |||
Db          3 NQTFITQFLLLGLPIPEEHQHLFYALFLVMYLTTILGNLLIIVLVQLDSQLHTPMYLFLS 62

Qy         65 NLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAYDRYV 124
              |||| |:| ||||:||:|: :  :  :| :  |: | :|  :|   | ||||: :||||||
Db         63 NLSFSDLCFSSVTMPKLLQNMRSQDTSIPYGGCLAQTYFFMVFGDMESFLLVAMAYDRYV 122

Qy        125 AICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCDVPLV 184
              ||| |||| ::|: ::|  ||  ||:  | |::  | |  || :|  |:: ::|||: ::
Db        123 AICFPLHYTSIMSPKLCTCLVLLLWMLTTSHAMMHTLLAARLSFCENNVVLNFFCDLFVL 182

Qy        185 IKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRK-HSAEGRQKALSTCSAH 243
              :||||:|||:  ::|   |  : :  |  :| ||  |: |: |  | :|  |  ||| :|
Db        183 LKLACSDTYINELMIFIMSTLLIIIPFFLIVMSYARIISSILKVPSTQGICKVFSTCGSH 242

Qy        244 FMVVALFFGPCIFIYTRP--DTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAM 298
              ||:||:|  | :|  |  : |   : |::: ||||||:|||||:||| ::| |:
Db        243 LSVVSLFYGTIIGLYLCPAGNNSTVKEMVMAMMYTVVTPMLNPFIYSLRNRDMKRAL 299


RESULT 6
F23701
olfactory receptor I7 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-Aug-1999
C;Accession: F23701
R;Buck, L.; Axel, R.
Cell 65, 175-187, 1991
A;Title: A novel multigene family may encode odorant receptors: a molecular basis for od
A;Reference number: A23701; MUID:91191556; PMID:1840504
A;Accession: F23701
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-327 <BUC>
A;Cross-references: GB:M64386; NID:g205833; PIDN:AAA41749.1; PID:g205834
C;Superfamily: olfactory receptor OR14
C;Keywords: G protein-coupled receptor; transmembrane protein

  Query Match             41.0%;  Score 660;  DB 2;  Length 327;
  Best Local Similarity   43.0%;  Pred. No. 2e-49;
  Matches  135;  Conservative   61;  Mismatches   98;  Indels   20;  Gaps    5;

Qy          1 MDSLNQT-RVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPM 59
              |:  | : ||:||| ||       | :| |       |:| |: |:|||||   |:||:||
Db          1 MERRNHSGRVSEFVLLGFPAPAPLRVLLFFLSLLXYVLVLTENMLIIIAIRNHPTLHKPM 60

Qy         60 YFFLSNLSFIDICHSSVTVPKMLEGLLLERKT----ISFDNCITQLFFLHLFACAEIFLL 115
              ||||:|:||::|  : :||:|||| | :  ::     |||: |:|||:|     | |  ||
Db         61 YFFLANMSFLEIWYVTVTIPKMLAGFIGSKENHGQLISFEACMTQLYFFLGLGCTECVLL 120

Qy        116 IIVAYDRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIID 175
               ::|||||||| ||||| ::: |:|:|:     | ||   |: : ||  || ||||| |:
Db        121 AVMAYDRYVAICHPLHYPVIVSSRLCVQMAAGSWAGGFGISMVKVFLISRLSYCGPNTIN 180

Qy        176 SYFCDVPLVIKLACTD-------TYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKH 228
              :||||  :: |:|||        ::  | |:    ::: : ::|:  : |      |

Db        181 HFFCDVSPLLNLSCTDMSTAELTDFVLAIFILLGPLSVTGASYMAITGAVM------RIP 234

Qy        229 SAEGRQKALSTCSAHFMVVALFFGPCIFIYTRPD--TSFSIDKVVSVFYTVVTPLLNPFI 286
              || || || |||::|  || :|:   |||| ||   ::|  :|:||| | |: || || |
Db        235 SAAGRHKAFSTCASHLTVVIIFYAASIFIYARPKALSAPDTNKLVSVLYAVIVPLFNPII 294

Qy        287 YTLRNEEVKSAMKQ 300
              | |||::|| |:::
Db        295 YCLRNQDVKRALRR 308


RESULT 7
A46247
olfactory receptor OR3 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 26-Aug-1999
C;Accession: A46247
R;Nef, P.; Hermans-Borgmeyer, I.; Artieres-Pin, H.; Beasley, L.; Dionne, V.E.; Heinemann
Proc. Natl. Acad. Sci. U.S.A. 89, 8948-8952, 1992
A;Title: Spatial pattern of receptor expression in the olfactory epithelium.
A;Reference number: A46247; MUID:93028384; PMID:1384038
A;Accession: A46247
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-312 <NEF>
A;Cross-references: GB:M84005; NID:g200153; PIDN:AAA39862.1; PID:g200154
A;Note: sequence extracted from NCBI backbone (NCBIP:115362)
C;Superfamily: olfactory receptor OR14

  Query Match             40.9%;  Score 659.5;  DB 2;  Length 312;
  Best Local Similarity   44.3%;  Pred. No. 2.1e-49;
  Matches  133;  Conservative   58;  Mismatches   92;  Indels   17;  Gaps    3;

Qy         12 FVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMYFFLSNLSFIDI 71
              |: :|::|:  ||::||    | |:||| ||: ||: :     |||||||||||| :|:
Db         12 FILMGVSDHPHLEIIFFAVILASYLLTLVGNLTIILLSRLDARLHTPMYFFLSNLSSLDL 71

Qy         72 CHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAYDRYVAICTPLH 131
               :: :||:||: |    ||||:  |:|||:          |  ||:::|:|||||:| |||
Db         72 AFTTSSVPQMLKNLWGPDKTISYGGCVTQLYVFLWLGATECILLVVMAFDRYVAVCRPLH 131

Qy        132 YPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCDVPLVIKLACTD 191
              |  ||| |:|  |    ||||  :|: |:  |::||:||   :|:: |:|| :||||| |
Db        132 YMTVMNPRLCWGLAAISWLGGLGNSVIQSTFTLQLPFCGHRKVDNFLCEVPAMIKLACGD 191

Qy        192 TYLTGILIVTNSGTISLSCFLAVVTSYMVILVS--------LRKHSAEGRQKALSTCSAH 243
              | |       |   ::  |     |||||         ::  | |||:|| :|| :|
Db        192 TSL-------NEAVLNGVCTFFTVVPVSVILVSYCFIAQAVMKIRSVEGRRKAFNTCVSH 244

Qy        244 FMVVALFFGPCIFIYTRP--DTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQL 301
              :|| ||:|  |: |  |   :: |  | :|:||:||||::|| ||||||:|| |: :|
Db        245 LVVVFLFYGSAIYGYLLPAKSSNQSQGKFISLFYSVVTPMVNPLIYTLRNKEVKGALGRL 304


RESULT 8
H23701
olfactory receptor I9 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-Aug-1999
C;Accession: H23701
R;Buck, L.; Axel, R.
Cell 65, 175-187, 1991
A;Title: A novel multigene family may encode odorant receptors: a molecular basis for od
A;Reference number: A23701; MUID:91191556; PMID:1840504
A;Accession: H23701
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-314 <BUC>
A;Cross-references: GB:M64388; NID:g205837; PIDN:AAA41751.1; PID:g205838
C;Superfamily: olfactory receptor OR14
C;Keywords: G protein-coupled receptor; transmembrane protein

  Query Match             40.9%;  Score 658.5;  DB 2;  Length 314;
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  Best Local Similarity   42.8%;  Pred. No. 2.6e-49;
  Matches  130;  Conservative   65;  Mismatches  106;  Indels    3;  Gaps    2;

Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              |   ||| :::|  |||      : ||:  | |:|: || ||::||| :    ||||||
Db          1 MTRRNQTAISQFFLLGLPFPPEYQHLFYALFLAMYLTTLLGNLIIIILILLDSHLHTPMY 60

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
               ||||||| |:| ||||:||:|: :  :  :| :  |: |::|   |     |||: :||
Db         61 LFLSNLSFADLCFSSVTMPKLLQNMQSQVPSIPYAGCLAQIYFFLFFGDLGNFLLVAMAY 120

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
              ||||||| |||| ::|: ::|: ||   |:  | |::  | |  || :|  ::|  ||||
Db        121 DRYVAICFPLHYMSIMSPKLCVSLVVLSWVLTTFHAMLHTLLMARLSFCEDSVIPHYFCD 180

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRK-HSAEGRQKALST 239
              :  ::|:||:||:   : |     | | :  || :: ||  |: |: |  |::   || ||
Db        181 MSTLLKVACSDTHDNELAIFILGGPIVVLPFLLIIVSYARIVSSIFKVPSSQSIHKAFST 240

Qy        240 CSAHFMVVALFFGPCIFIYTRPDTSFSIDK--VVSVFYTVVTPLLNPFIYTLRNEEVKSA 297
              | :|  ||:||:|  | :|  |  : |  |  |:|: ||:|||:|||||:||| ::| |
Db        241 CGSHLSVVSLFYGTVIGLYLCPSANNSTVKETVMSLMYTMVTPMLNPFIYSLRNRDIKDA 300

Qy        298 MKQL 301
              ::::
Db        301 LEKI 304


RESULT 9
S51356
olfactory receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S51356; S47014
R;Gat, U.; Nekrasova, E.; Lancet, D.; Natochin, M.
Eur. J. Biochem. 225, 1157-1168, 1994
A;Title: Olfactory receptor proteins. Expression, characterization and partial purificat
A;Reference number: S51356; MUID:95045546; PMID:7957207
A;Accession: S51356
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-309 <GAT>
A;Cross-references: EMBL:X80671; NID:g517365; PIDN:CAA56697.1; PID:g517366
R;Gat, U.; Nekrasova, E.; Lancet, D.; Natochin, M.
submitted to the EMBL Data Library, July 1994
A;Description: Olfactory receptor proteins: expression, characterization and partial pur
A;Reference number: S47014
A;Accession: S47014
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-309 <GA2>
A;Cross-references: EMBL:X80671; NID:g517365; PIDN:CAA56697.1; PID:g517366
C;Superfamily: olfactory receptor OR14

  Query Match             40.8%;  Score 657.5;  DB 1;  Length 309;
  Best Local Similarity   44.3%;  Pred. No. 3.1e-49;
  Matches  136;  Conservative   56;  Mismatches  112;  Indels    3;  Gaps    2;

Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              | : | : |  || :|||    | :  |  |  ||:||: ||: :|:  : :| ||||||
Db          2 MGTGNHSAVVVFVLVGLTKQPELLLPLFFLFLVIYVLTVVGNLGMILLIIVSPLLHTPMY 61

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
              :|||:|||:|:|:|:|  ||||   | ::  |::  |: | ||  :|   | :|| ::||
Db         62 YFLSSLSFVDLCYSTVITPKMLVNFLGKKNFITYSECMAQFFFFAIFVVTEGYLLTVMAY 121

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
              ||||||| || |  :|: |:|  ||   :  |   ::  |   : | :|   || ||||
Db        122 DRYVAICRPLLYNVIMSSRICSLLVLVAFSLGLFSAVVHTSAMMNLSFCKSYIISHYFCD 181

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVS-LRKHSAEGRQKALST 239
                 ::||||::|:|  :||     |  :|   |||  ||: |  | ||  |:||| ||  |
Db        182 ALPLLKLACSNTHLNELLIFIIGGLNTLVPTLAVAISYVFIFCSILRIRSSEGRSKAFGT 241
```

```
Qy        240 CSAHFMVVALFFGPCIFIYTRPDTSFSI--DKVVSVFYTVVTPLLNPFIYTLRNEEVKSA 297
              ||:| | | :|||   |:| :| :|  |:  :|| ||||| | |:||| ||:|||::|| |
Db        242 CSSHLMAVGIFFGSITFMYLKPSSSNSLEQEKVSSVFYTTVIPMLNPLIYSLRNKDVKKA 301

Qy        298 MKQLRQR 304
              : :   |
Db        302 LGRFSVR 308


RESULT 10
S20572
olfactory receptor - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 26-Aug-1999
C;Accession: S20572
R;Parmentier, M.; Libert, F.; Schurmans, S.; Schiffmann, S.; Lefort, A.; Eggerickx, D.;
Nature 355, 453-455, 1992
A;Title: Expression of members of the putative olfactory receptor gene family in mammali
A;Reference number: S20571; MUID:92131132; PMID:1370859
A;Accession: S20572
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-314 <PAR>
A;Cross-references: EMBL:X64994; NID:g32085; PIDN:CAA46127.1; PID:g32086
C;Superfamily: olfactory receptor OR14
C;Keywords: G protein-coupled receptor; transmembrane protein

  Query Match             40.7%;  Score 656;  DB 2;  Length 314;
  Best Local Similarity   43.4%;  Pred. No. 4.2e-49;
  Matches  134;  Conservative   67;  Mismatches  104;  Indels    4;  Gaps    3;

Qy          5 NQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMYFFLS 64
              ||| :::|: |||      : | :  | |:|: || ||:|||:       |||||| |||
Db          5 NQTSISDFLLLGLPIQPEQQNLCYALFLAMYLTTLLGNLLIIVLIRLDSHLHTPMYLFLS 64

Qy         65 NLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAYDRYV 124
              |||| |:| ||||:||:|: :  :  :| : :|:||::|  ||   | |||: :||||||
Db         65 NLSFSDLCFSSVTIPKLLQNMQNQDPSIPYADCLTQMYFFLLFGDLESFLLVAMAYDRYV 124

Qy        125 AICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCDVPLV 184
              ||| ||||  :|:  :|: ||    |:  | |::  | |  || :|  |:|  :|||:  :
Db        125 AICFPLHYTAIMSPMLCLALVALSWVLTTFHAMLHTLLMARLCFCADNVIPHFFCDMSAL 184

Qy        185 IKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRK-HSAEGRQKALSTCSAH 243
              :||| :|| :   :|    | | :  || :: ||  |: |: |  |::|  || ||| :|
Db        185 LKLAFSDTRVNEWVIFIMGGLILVIPFLLILGSYARIVSSILKVPSSKGICKAFSTCGSH 244

Qy        244 FMVVALFFGPCIFIY--TRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ- 300
              ||:||:|  | :|  :  ::|   | |::: ||||||:||||||:||| ::| |: :
Db        245 LSVVSLFYGTVIGLYLCSSANSSTLKDTVMAMMYTVVTPMLNPFIYSLRNRDMKGALSRV 304

Qy        301 LRQRQVFFT 309
              : |:: ||:
Db        305 IHQKKTFFS 313


RESULT 11
A37286
olfactory receptor I15 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-Aug-1999
C;Accession: A37286
R;Buck, L.; Axel, R.
Cell 65, 175-187, 1991
A;Title: A novel multigene family may encode odorant receptors: a molecular basis for od
A;Reference number: A23701; MUID:91191556; PMID:1840504
A;Accession: A37286
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-314 <BUC>
A;Cross-references: GB:M64392; NID:g205845; PIDN:AAA41755.1; PID:g205846
C;Superfamily: olfactory receptor OR14
```

C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 40.7%; Score 656; DB 2; Length 314;
Best Local Similarity 41.7%; Pred. No. 4.2e-49;
Matches 130; Conservative 71; Mismatches 107; Indels 4; Gaps 3;

```
Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              |   ||| :::|: | |       : :|:  | ::|: |: ||::|||         ||||||
Db          1 MTEENQTVISQFLLLFLPIPSEHQHVFYALFLSMYLTTVLGNLIIIILIHLDSHLHTPMY 60

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
               ||||||| |:| ||||:||:|: :  :  :| |  |:|||:|   ||  | |||: :||
Db         61 LFLSNLSFSDLCFSSVTMPKLLQNMQSQVPSIPFAGCLTQLYFYLYFADLESFLLVAMAY 120

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
               ||||||| |||| ::|: ::|: ||   |:  | |::  | |  || :|  |:|  :|||
Db        121 DRYVAICFPLHYMSIMSPKLCVSLVVLSWVLTTFHAMLHTLLMARLSFCADNMIPHFFCD 180

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRK-HSAEGRQKALST 239
              :  ::||:|:||::  ::|    | : :  |: :: ||  :: |: |  |  |  |  ||
Db        181 ISPLLKLSCSDTHVNELVIFVMGGLVIVIPFVLIIVSYARVVASILKVPSVRGIHKIFST 240

Qy        240 CSAHFMVVALFFGPCIFIYTRPDTSFSIDK--VVSVFYTVVTPLLNPFIYTLRNEEVKSA 297
              | :|  ||:||:|  | :|  |  : |  |  |::: ||||||:||||||:||| ::| |
Db        241 CGSHLSVVSLFYGTIIGLYLCPSANNSTVKETVMAMMYTVVTPMLNPFIYSLRNRDMKEA 300

Qy        298 M-KQLRQRQVFF 308
              : : | :::: |
Db        301 LIRVLCKKKITF 312
```

RESULT 12
S20571
olfactory receptor - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 26-Aug-1999
C;Accession: S20571
R;Parmentier, M.; Libert, F.; Schurmans, S.; Schiffmann, S.; Lefort, A.; Eggerickx, D.;
Nature 355, 453-455, 1992
A;Title: Expression of members of the putative olfactory receptor gene family in mammali
A;Reference number: S20571; MUID:92131132; PMID:1370859
A;Accession: S20571
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-313 <PAR>
A;Cross-references: EMBL:X64996; NID:g890; PIDN:CAA46129.1; PID:g891
C;Superfamily: olfactory receptor OR14
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 40.7%; Score 655; DB 2; Length 313;
Best Local Similarity 44.1%; Pred. No. 5.1e-49;
Matches 134; Conservative 61; Mismatches 105; Indels 4; Gaps 3;

```
Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              |   ||| |:||| |||  :     ||:  | |:|: |: ||:|||:        ||||||
Db          1 MTEKNQTVVSEFVLLGLPIDPDQRDLFYALFLAMYVTTILGNLLIIVLIQLDSHLHTPMY 60

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
               ||||||| |:| ||||:||:|: :  :  :| :  |:||::|    |  | |||: :||
Db         61 LFLSNLSFSDLCFSSVTMPKLLQNMQSQVPSIPYAGCLTQMYFFLFFGDLESFLLVAMAY 120

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
               ||||||| ||||  :|: ::|   |:   |:    |::  | |  || :|  | |  :|||
Db        121 DRYVAICFPLHYTTIMSPKLCFSLLVLSWVLTMFHAVLHTLLMARLCFCA-NTIPHFFCD 179

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRK-HSAEGRQKALST 239
              :  ::||||:||  :  ::|     | | :  || ::|||   |: |: |  || |  |  ||
Db        180 MSALLKLACSDTQVNELVIFIMGGLILVIPFLLIITSYARIVSSILKVPSAIGICKVFST 239

Qy        240 CSAHFMVVALFFGPCIFIYTRPDTSFSIDK--VVSVFYTVVTPLLNPFIYTLRNEEVKSA 297
              | :|  ||:||:|  | :|  |  : |  |  |::: ||||||:|||||:|||:::| |
Db        240 CGSHLSVVSLFYGTVIGLYLCPSANNSTVKETIMAMMYTVVTPMLNPFIYSLRNKDMKGA 299

Qy        298 MKQL 301
              ::::
Db        300 LRRV 303
```

RESULT 13
I23701
olfactory receptor I14 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-Aug-1999
C;Accession: I23701
R;Buck, L.; Axel, R.
Cell 65, 175-187, 1991
A;Title: A novel multigene family may encode odorant receptors: a molecular basis for o
A;Reference number: A23701; MUID:91191556; PMID:1840504
A;Accession: I23701
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-312 <BUC>
A;Cross-references: GB:M64391; NID:g205843; PIDN:AAA41754.1; PID:g205844
C;Superfamily: olfactory receptor OR14
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 40.6%; Score 653.5; DB 2; Length 312;
Best Local Similarity 43.5%; Pred. No. 6.9e-49;
Matches 131; Conservative 55; Mismatches 112; Indels 3; Gaps 2;

```
Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              |   ||| : ||: |||        :||:  | |:|:  : ||:|||:        || |||
Db          1 MTGNNQTLILEFLLLGLPIPSEYHLLFYALFLAMYLTIILGNLLIIVLVRLDSHLHMPMY 60

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
               ||||||| |:| ||||:||:|: :  :  :||:  |:|||:|  :|   | |||:::||
Db         61 LFLSNLSFSDLCFSSVTMPKLLQNMQSQVPSISYTGCLTQLYFFMVFGDMESFLLVVMAY 120

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
               ||||||| || |  :|: : |  ||  ||:     |:|  | |  || :|  |:|  :|||
Db        121 DRYVAICFPLRYTTIMSTKFCASLVLLLWMLTMTHALLHTLLIARLSFCEKNVILHFFCD 180

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKH-SAEGRQKALST 239
              :  ::||:|:|  |:  ::|     | | :  || :| ||: |  |: |  | :    | ||
Db        181 ISALLKLSCSDIYVNELMIYILGGLIIIIPFLLIVMSYVRIFFSILKFPSIQDIYKVFST 240

Qy        240 CSAHFMVVALFFGPCIFIYTRPDTSFSIDK--VVSVFYTVVTPLLNPFIYTLRNEEVKSA 297
              | :|  || ||:|     ||  |  : |  |   ::: ||||||:||||||:||| ::| |
Db        241 CGSHLSVVTLFYGTIFGIYLCPSGNNSTVKEIAMAMMYTVVTPMLNPFIYSLRNRDMKRA 300

Qy        298 M 298
              :
Db        301 L 301
```

RESULT 14
S29711
olfactory factor OR37 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 04-Sep-1998
C;Accession: S29711
R;Raming, K.; Krieger, J.; Strotmann, J.; Boekhoff, I.; Kubick, S.; Baumstark, C.; Breer
Nature 361, 353-356, 1993
A;Title: Cloning and expression of odorant receptors.
A;Reference number: S29707; MUID:93149273; PMID:7678922
A;Accession: S29711
A;Molecule type: mRNA
A;Residues: 1-305 <RAM>
C;Superfamily: olfactory receptor OR14

Query Match 40.0%; Score 645; DB 2; Length 305;
Best Local Similarity 42.1%; Pred. No. 3.6e-48;
Matches 128; Conservative 68; Mismatches 98; Indels 10; Gaps 3;

```
Qy         13 VFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMYFFLSNLSFIDIC 72
              : |||:     |:|:|:    :|::  :|| ::|||::|   |||||||| ||||:|||
```

```
Db          1 LLLGLSGYPKTEILYFVIVLVMYLVIHTGNGVLIIASIFDSHLHTPMYFFLGNLSFLDIC 60

Qy         73 HSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAYDRYVAICTPLHY 132
              ::: :||  |  |: ::: |||  |  |:|         |  || ::|:|||||| || |
Db         61 YTTSSVPSTLVSLISKKRNISFSGCTVQMFVGFAMGSTECLLLGMMAFDRYVAICNPLRY 120

Qy        133 PNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCDVPLVIKLACTDT 192
              :|:  | : :  | |  | ::|: || | :|||:|| |:|: : |:|  |:|||| |
Db        121 SVIMSKEVYVSMASASWFSGGINSVVQTSLAMRLPFCGNNVINHFTCEVLAVLKLACADI 180

Qy        193 YLTGILIVTNSGTISLSCFLAVVTSYMVILVS-LRKHSAEGRQKALSTCSAHFMVVALFF 251
               |  : :| ::    :   | :  ||::|| : || :|| ||:|| |||||  || :|:
Db        181 SLNIVTMVISNMAFLVLPLLLIFFSYVLILYTILRMNSASGRRKAFSTCSAHLTVVVIFY 240

Qy        252 GPCIFIYTRP--------DTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ-LR 302
              |    :| :|        |   : ||::|:|| |||||||| ||:|||::||:|:|  |:
Db        241 GTIFSMYAKPKSQDLTGKDKFQTSDKIISLFYGVVTPMLNPIIYSLRNKDVKAAVKYILK 300

Qy        303 QRQV 306
              |: :
Db        301 QKYI 304


RESULT 15
JC5200
chemoreceptor TB334 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 26-Aug-1999
C;Accession: JC5200; PC4302
R;Thomas, M.B.; Haines, S.L.; Akeson, R.A.
Gene 178, 1-5, 1996
A;Title: Chemoreceptors expressed in taste, olfactory and male reproductive tissues.
A;Reference number: JC5200; MUID:97080538; PMID:8921883
A;Accession: JC5200
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-311 <THO1>
A;Cross-references: GB:U50947; NID:g1256388; PIDN:AAC52909.1; PID:g1256389
A;Accession: PC4302
A;Status: preliminary
A;Molecule type: protein
A;Residues: 146-153;265-272 <THO2>
A;Experimental source: taste bud
C;Comment: This protein is coupled to a GTP-binding protein-mediated signal transduction
C;Genetics:
A;Gene: tb334
C;Superfamily: olfactory receptor OR14
C;Keywords: olfaction; taste bud; transmembrane protein
F;24-47/Domain: transmembrane #status predicted <TM1>
F;56-77/Domain: transmembrane #status predicted <TM2>
F;99-118/Domain: transmembrane #status predicted <TM3>
F;138-162/Domain: transmembrane #status predicted <TM4>
F;195-217/Domain: transmembrane #status predicted <TM5>
F;236-258/Domain: transmembrane #status predicted <TM6>
F;271-291/Domain: transmembrane #status predicted <TM7>

  Query Match             40.0%;  Score 644.5;  DB 2;  Length 311;
  Best Local Similarity   42.3%;  Pred. No. 4.1e-48;
  Matches  127;  Conservative   65;  Mismatches  105;  Indels    3;  Gaps    2;

Qy          5 NQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMYFFLS 64
              ||: |:||   |::     : | :  |  :|::||:||:|||:|    | |||||||||:
Db          3 NQSSVSEFFLRGISGFPEQQQLLYGLFLCMYLVTLTGNVLIILAIGSDPHLHTPMYFFLA 62

Qy         65 NLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAYDRYV 124
              |||| |:   | || |||  :  :  |||:  |:||::   :|   : | | ::||||||
Db         63 NLSFADMGLISSTVTKMLFNVQTQCHTISYTGCLTQMYLFMMFGDLDSFFLAVMAYDRYV 122

Qy        125 AICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCDVPLV 184
              ||| ||||  :|| |:|: ::   |:   | :|  | |  || :|    |  :||||  |
Db        123 AICHPLHYSTIMNARICVLMLILCWILTNVVALTHTLLMARLSFCVVGEIAHFFCDVTSV 182

Qy        185 IKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYM-VILVSLRKHSAEGRQKALSTCSAH 243
              :||:|:||::  :::    ||: :  |:::| ||: ::   ||  |: |  || ||||:|
Db        183 MKLSCSDTHVNELVLSGFGGTVLMVPFVSIVISYVHIVFAVLRIQSSGGSSKAFSTCSSH 242

Qy        244 FMVVALFFGPCIFIYTRPDTSFSIDKVV--SVFYTVVTPLLNPFIYTLRNEEVKSAMKQL 301
              || :|:|    :|  | :  : :| |  :  ||||||:||||||:|||:::| |:|:|
Db        243 LCVVCVFYGTLFSVYLFPSSVETTEKDVAAAAMYTVVTPMLNPFIYSLRNKDIKGALKRL 302


Search completed: August 12, 2003, 16:09:46
Job time : 40 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 12, 2003, 16:06:51 ; Search time 24 Seconds
(without alignments)
1660.142 Million cell updates/sec

Title: US-09-807-132-4
Perfect score: 1611
Sequence: 1 MDSLNQTRVTEFVFLGLTDN.....VKSAMKQLRQRQVFFTKSYT 313

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 479057 seqs, 127295195 residues

Total number of hits satisfying chosen parameters: 479057

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1611	100.0	313	12	US-10-017-161-426	Sequence 426, App
2	1611	100.0	313	15	US-10-220-382-7	Sequence 7, Appli
3	1380	85.7	308	11	US-09-832-522-82	Sequence 82, Appl
4	1377	85.5	305	9	US-09-761-288-86	Sequence 86, Appl
5	1377	85.5	305	11	US-09-898-586-86	Sequence 86, Appl
6	1271	78.9	280	11	US-09-800-321A-54	Sequence 54, Appl
7	938	58.2	311	10	US-09-886-055-309	Sequence 309, App
8	938	58.2	311	11	US-09-804-291-309	Sequence 309, App
9	929	57.7	314	10	US-09-886-055-403	Sequence 403, App
10	929	57.7	314	11	US-09-804-291-403	Sequence 403, App
11	929	57.7	314	12	US-10-017-161-402	Sequence 402, App
12	927.5	57.6	310	10	US-09-886-055-447	Sequence 447, App
13	927.5	57.6	310	11	US-09-804-291-447	Sequence 447, App
14	919	57.0	324	15	US-10-023-601-34	Sequence 34, Appl
15	919	57.0	348	10	US-09-886-055-409	Sequence 409, App
16	919	57.0	348	11	US-09-804-291-409	Sequence 409, App
17	919	57.0	348	12	US-10-017-161-396	Sequence 396, App
18	905	56.2	325	10	US-09-886-055-405	Sequence 405, App
19	905	56.2	325	11	US-09-804-291-405	Sequence 405, App
20	900	55.9	305	9	US-09-761-288-85	Sequence 85, Appl
21	900	55.9	305	11	US-09-898-586-85	Sequence 85, Appl
22	900	55.9	318	9	US-09-761-288-20	Sequence 20, Appl
23	900	55.9	318	10	US-09-886-055-79	Sequence 79, Appl
24	900	55.9	318	11	US-09-898-586-20	Sequence 20, Appl
25	900	55.9	318	11	US-09-804-291-79	Sequence 79, Appl
26	900	55.9	318	15	US-10-220-382-21	Sequence 21, Appl
27	893	55.4	302	11	US-09-800-321A-52	Sequence 52, Appl
28	893	55.4	311	12	US-10-017-161-398	Sequence 398, App
29	889	55.2	308	10	US-09-886-055-237	Sequence 237, App
30	889	55.2	308	11	US-09-804-291-237	Sequence 237, App
31	889	55.2	308	12	US-10-017-161-414	Sequence 414, App
32	888	55.1	311	10	US-09-886-055-401	Sequence 401, App
33	888	55.1	311	11	US-09-804-291-401	Sequence 401, App
34	888	55.1	311	12	US-10-017-161-390	Sequence 390, App
35	878	54.5	343	10	US-09-886-055-239	Sequence 239, App
36	878	54.5	343	11	US-09-804-291-239	Sequence 239, App
37	878	54.5	343	12	US-10-017-161-416	Sequence 416, App
38	871	54.1	234	10	US-09-746-284-4	Sequence 4, Appli
39	869	53.9	308	11	US-09-800-321A-51	Sequence 51, Appl
40	869	53.9	310	12	US-10-017-161-268	Sequence 268, App
41	866	53.8	286	11	US-09-800-321A-25	Sequence 25, Appl
42	866	53.8	313	10	US-09-886-055-407	Sequence 407, App
43	866	53.8	313	11	US-09-804-291-407	Sequence 407, App
44	865	53.7	292	12	US-10-017-161-504	Sequence 504, App
45	865	53.7	307	12	US-10-017-161-406	Sequence 406, App

ALIGNMENTS

RESULT 1
US-10-017-161-426
; Sequence 426, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 426
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-161-426

Query Match 100.0%; Score 1611; DB 12; Length 313;
Best Local Similarity 100.0%; Pred. No. 2.1e-148;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
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Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTC 240
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Db        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTC 240

Qy        241 SAHFMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SAHFMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300

Qy        301 LRQRQVFFTKSYT 313
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Db        301 LRQRQVFFTKSYT 313


RESULT 2
US-10-220-382-7
; Sequence 7, Application US/10220382
; Publication No. US20030119111A1
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.
;  APPLICANT:  LAL, Preeti
;  APPLICANT:  TANG, Y. Tom
;  APPLICANT:  PATTERSON, Chandra
;  APPLICANT:  YAO, Monique G.
;  APPLICANT:  SHIH, Leo L.
;  APPLICANT:  TRIBOULEY, Catherine
;  APPLICANT:  LU, Dyung Aina M.
;  APPLICANT:  YUE, Henry
;  APPLICANT:  KHAN, Farrah A.
;  APPLICANT:  POLICKY, Jennifer L.
;  APPLICANT:  AU-YOUNG, Janice
;  APPLICANT:  YANG, Junming
;  APPLICANT:  HARLAND, Lee
;  APPLICANT:  WALSH, Roderick T.
;  APPLICANT:  LO, Terence P.
;  APPLICANT:  BOROWSKY, Mark L.
;  TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
;  FILE REFERENCE: PI-0044 PCT
;  CURRENT APPLICATION NUMBER: US/10/220,382
;  CURRENT FILING DATE:  2001-03-01
;  PRIOR APPLICATION NUMBER: 60/186,854; 60/188,384; 60/190,453; 60/190,730
;  PRIOR FILING DATE: 2000-03-03; 2000-03-10; 2000-03-17; 2000-03-20
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PERL Program
; SEQ ID NO 7
;   LENGTH: 313
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20030119111A1 3082743CD1
US-10-220-382-7

  Query Match            100.0%;  Score 1611;  DB 15;  Length 313;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-148;
  Matches  313;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTC 240

Qy        241 SAHFMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SAHFMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300

Qy        301 LRQRQVFFTKSYT 313
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Db        301 LRQRQVFFTKSYT 313


RESULT 3
US-09-832-522-82
; Sequence 82, Application US/09832522
; Publication No. US20030091563A1
; GENERAL INFORMATION:
;  APPLICANT: Shenoy, Suresh G
;  APPLICANT:  Gangolli, Esha A
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Smithson, Glennda
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  Wolenc, Adam R
;  APPLICANT:  Casman, Stacie J
;  APPLICANT:  Tchernev, Velizar T
;  APPLICANT:  Szekeres, Edward S
;  APPLICANT:  Grosse, William
;  APPLICANT:  Alsobrook, John P
;  APPLICANT:  Burgess, Catherine E
;  TITLE OF INVENTION: No. US20030091563A1el GPCR-Proteins and Nucleic Acids Encoding S
;  FILE REFERENCE: 15966-767
;  CURRENT APPLICATION NUMBER: US/09/832,522
;  CURRENT FILING DATE:  2001-04-11
;  PRIOR APPLICATION NUMBER: 60/195,994
;  PRIOR FILING DATE: 2000-04-11
;  PRIOR APPLICATION NUMBER: 60/196,538
;  PRIOR FILING DATE: 2000-04-11
;  PRIOR APPLICATION NUMBER: 60/220,644
;  PRIOR FILING DATE: 2000-07-25
;  PRIOR APPLICATION NUMBER: 60/264,851
;  PRIOR FILING DATE: 2001-01-29
;  PRIOR APPLICATION NUMBER: 60/199,964
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: 60/268,567
;  PRIOR FILING DATE: 2001-02-14
;  PRIOR APPLICATION NUMBER: 60/199,955
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: 60/259,641
;  PRIOR FILING DATE: 2001-01-04
;  PRIOR APPLICATION NUMBER: 60/200,176
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: 60/199,948
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: 60/199,956
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: 60/218,995
;  PRIOR FILING DATE: 2000-07-17
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
;   LENGTH: 308
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-832-522-82

  Query Match            85.7%;  Score 1380;  DB 11;  Length 308;
  Best Local Similarity   85.6%;  Pred. No. 5.6e-126;
  Matches  262;  Conservative   20;  Mismatches   24;  Indels    0;  Gaps    0;

Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              | :|||||||||:|||||| |||:|||: |:  ||||| || ||::  |||| || |||
Db          1 MGALNQTRVTEFIFLGLTDNWVLEILFFVPFTVTYMLTLLGNFLIVVTIVFTPRLHNPMY 60

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
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Db         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCIAQLFFLHLFACSEIFLLTIMAY 120

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
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Db        121 DRYVAICIPLHYSNVMNMKVCVQLVFALWLGGTIHSLVQTFLTIRLPYCGPNIIDSYFCD 180

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTC 240
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Db        181 VPPVIKLACTDTYLTGILIVSNSGTISLVCFLALVTSYTVILFSLRKKSAEGRRKALSTC 240

Qy        241 SAHFMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300
              ||||||| ||||||||:|||||:||||||||||||||||||||| ||||||||||:|||
Db        241 SAHFMVVTLFFGPCIFLYTRPDSSFSIDKVVSVFYTVVTPLLNPLIYTLRNEEVKTAMKH 300

Qy        301 LRQRQV 306
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Db        301 LRQRRI 306


RESULT 4
US-09-761-288-86
; Sequence 86, Application US/09761288
; Patent No. US20020065405A1
; GENERAL INFORMATION:
;  APPLICANT: Padigaru, Muralidhara
;  APPLICANT:  Prayaga, Sudhirdas
;  APPLICANT:  Taupier, Raymond J
;  APPLICANT:  Mishra, Vishnu
;  APPLICANT:  Tchernev, Velizar
;  APPLICANT:  Spytek, Kimberky
;  APPLICANT:  Li, Li
;  TITLE OF INVENTION: No. US20020065405A1el Polypeptides and Nucleic Acids Encoding Sam
;  FILE REFERENCE: 15966-638
;  CURRENT APPLICATION NUMBER: US/09/761,288
;  CURRENT FILING DATE:  2001-01-16
;  PRIOR APPLICATION NUMBER: 60/177,839
;  PRIOR FILING DATE: 2000-01-25
;  PRIOR APPLICATION NUMBER: 60/176,134
;  PRIOR FILING DATE: 2000-01-14
;  PRIOR APPLICATION NUMBER: 60/175,989
;  PRIOR FILING DATE: 2000-01-13
;  PRIOR APPLICATION NUMBER: 60/218,324
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: 60/220,253
;  PRIOR FILING DATE: 2000-07-24
;  PRIOR APPLICATION NUMBER: 60/178,191
;  PRIOR FILING DATE: 2000-01-26
;  PRIOR APPLICATION NUMBER: 60/178,227
;  PRIOR FILING DATE: 2000-01-26
;  PRIOR APPLICATION NUMBER: 60/220,590
;  PRIOR FILING DATE: 2000-07-25
;  NUMBER OF SEQ ID NOS: 95
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 86
;   LENGTH: 305
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-761-288-86

  Query Match           85.5%;  Score 1377;  DB 9;  Length 305;
  Best Local Similarity   85.9%;  Pred. No. 1.1e-125;
  Matches  262;  Conservative   19;  Mismatches   24;  Indels    0;  Gaps    0;

Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              | :|||||||||:|||||| |||:|||: |:  ||||| || ||::  |||| || |||
Db          1 MGALNQTRVTEFIFLGLTDNWVLEILFFVPFTVTYMLTLLGNFLIVVTIVFTPRLHNPMY 60

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
              ||||||||||||||||||||||||||||||||||| |||||||||:||||| |:||
Db         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCIAQLFFLHLFACSEIFLLTIMAY 120

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
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Db        121 DRYVAICIPLHYSNVMNMKVCVQLVFALWLGGTIHSLVQTFLTIRLPYCGPNIIDSYFCD 180

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTC 240
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Db        181 VPPVIKLACTDTYLTGILIVSNSGTISLVCFLALVTSYTVILFSLRKKSAEGRRKALSTC 240

Qy        241 SAHFMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300
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Db        241 SAHFMVVTLFFGPCIFLYTRPDSSFSIDKVVSVFYTVVTPLLNPLIYTLRNEEVKTAMKH 300

Qy        301 LRQRQ 305
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Db        301 LRQRR 305


RESULT 5
US-09-898-586-86
; Sequence 86, Application US/09898586
; Publication No. US20030077794A1
; GENERAL INFORMATION:
;  APPLICANT: Gerlach, Valerie L
;  APPLICANT:  MacDougall, John R
;  APPLICANT:  Smithson, Glennda
;  TITLE OF INVENTION: No. US20030077794A1el Polypeptides and Nucleic Acids Encoding Sa
;  FILE REFERENCE: 15966-638CIP
;  CURRENT APPLICATION NUMBER: US/09/898,586
;  CURRENT FILING DATE:  2001-08-27
;  PRIOR APPLICATION NUMBER: 60/177,839
;  PRIOR FILING DATE: 2000-01-25
;  PRIOR APPLICATION NUMBER: 60/176,134
;  PRIOR FILING DATE: 2000-01-14
;  PRIOR APPLICATION NUMBER: 60/175,989
;  PRIOR FILING DATE: 2000-01-13
;  PRIOR APPLICATION NUMBER: 60/218,324
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: 60/220,253
;  PRIOR FILING DATE: 2000-07-24
;  PRIOR APPLICATION NUMBER: 60/178,191
;  PRIOR FILING DATE: 2000-01-26
;  PRIOR APPLICATION NUMBER: 60/178,227
;  PRIOR FILING DATE: 2000-01-26
;  PRIOR APPLICATION NUMBER: 60/220,590
;  PRIOR FILING DATE: 2000-07-25
;  PRIOR APPLICATION NUMBER: 09/761,288
;  PRIOR FILING DATE: 2001-01-16
;  NUMBER OF SEQ ID NOS: 104
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
;   LENGTH: 305
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-898-586-86

  Query Match           85.5%;  Score 1377;  DB 11;  Length 305;
  Best Local Similarity   85.9%;  Pred. No. 1.1e-125;
  Matches  262;  Conservative   19;  Mismatches   24;  Indels    0;  Gaps    0;

Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              | :|||||||||:|||||| |||:|||: |:  ||||| || ||::  |||| || |||
Db          1 MGALNQTRVTEFIFLGLTDNWVLEILFFVPFTVTYMLTLLGNFLIVVTIVFTPRLHNPMY 60

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
              ||||||||||||||||||||||||||||||||||| |||||||||:||||| |:||
Db         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCIAQLFFLHLFACSEIFLLTIMAY 120

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
              ||||||| |||| |||||:||:||||||||||||:||| ||||||||||||||||||||||
Db        121 DRYVAICIPLHYSNVMNMKVCVQLVFALWLGGTIHSLVQTFLTIRLPYCGPNIIDSYFCD 180

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTC 240
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Db        181 VPPVIKLACTDTYLTGILIVSNSGTISLVCFLALVTSYTVILFSLRKKSAEGRRKALSTC 240
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Qy        241 SAHFMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300
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Db        241 SAHFMVVTLFFGPCIFLYTRPDSSFSIDKVVSVFYTVVTPLLNPLIYTLRNEEVKTAMKH 300

Qy        301 LRQRQ 305
              ||||:
Db        301 LRQRR 305


RESULT 6
US-09-800-321A-54
; Sequence 54, Application US/09800321A
; Publication No. US20030068671A1
; GENERAL INFORMATION:
;  APPLICANT: Padigaru, Muralidhara
;  APPLICANT:  Burgess, Catherine E
;  APPLICANT:  Mishra, Vishnu
;  APPLICANT:  Li, Li
;  APPLICANT:  Baumgartner, Jason C
;  APPLICANT:  Majumder, Kumud
;  APPLICANT:  Spytek, Kimberly A
;  APPLICANT:  Tchernev, Velizar T
;  TITLE OF INVENTION: No. US20030068671A1el Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 15966-703 US
;  CURRENT APPLICATION NUMBER: US/09/800,321A
;  CURRENT FILING DATE:  2001-03-05
;  PRIOR APPLICATION NUMBER: 60/186,606
;  PRIOR FILING DATE: 2000-03-03
;  PRIOR APPLICATION NUMBER: 60/221,942
;  PRIOR FILING DATE: 2000-07-31
;  PRIOR APPLICATION NUMBER: 60/260,285
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: 60/220,263
;  PRIOR FILING DATE: 2000-07-24
;  PRIOR APPLICATION NUMBER: 60/257,600
;  PRIOR FILING DATE: 2000-12-21
;  PRIOR APPLICATION NUMBER: 60/187,295
;  PRIOR FILING DATE: 2000-03-06
;  PRIOR APPLICATION NUMBER: 60/219,854
;  PRIOR FILING DATE: 2000-07-21
;  PRIOR APPLICATION NUMBER: 60/187,249
;  PRIOR FILING DATE: 2000-03-06
;  PRIOR APPLICATION NUMBER: 60/187,247
;  PRIOR FILING DATE: 2000-03-06
;  PRIOR APPLICATION NUMBER: 60/187,250
;  PRIOR FILING DATE: 2000-03-06
;  PRIOR APPLICATION NUMBER: 60/187,253
;  PRIOR FILING DATE: 2000-03-06
;  PRIOR APPLICATION NUMBER: 60/187,248
;  PRIOR FILING DATE: 2000-03-06
;  PRIOR APPLICATION NUMBER: 60/187,296
;  PRIOR FILING DATE: 2000-03-06
;  PRIOR APPLICATION NUMBER: 60/187,563
;  PRIOR FILING DATE: 2000-03-07
;  NUMBER OF SEQ ID NOS: 78
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
;   LENGTH: 280
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-800-321A-54

  Query Match             78.9%;  Score 1271;  DB 11;  Length 280;
  Best Local Similarity   86.1%;  Pred. No. 1.9e-115;
  Matches  241;  Conservative   17;  Mismatches   22;  Indels    0;  Gaps    0;

Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              | :|||||||||:|||||| |||:|||: |:  ||||| || ||::  |||| || |||
Db          1 MGALNQTRVTEFIFLGLTDNWVLEILFFVPFTVTYMLTLLGNFLIVVTIVFTPRLHNPMY 60

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
              |||||||||||||||||||||||||||||||||||| ||||||||||:||||| |:||
Db         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCIAQLFFLHLFACSEIFLLTIMAY 120

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
              ||||||| |||| ||||:||:||||||||||:||| |||||||||||||||||||||||
Db        121 DRYVAICIPLHYSNVMNMKVCVQLVFALWLGGTIHSLVQTFLTIRLPYCGPNIIDSYFCD 180

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTC 240
              || |||||||||||||||:||||||| ||||:|||| ||| |||| |||||:||||||
Db        181 VPPVIKLACTDTYLTGILIVSNSGTISLVCFLALVTSYTVILFSLRKKSAEGRRKALSTC 240

Qy        241 SAHFMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTP 280
              ||||||| ||||||||:|||||:||||||||||||||||
Db        241 SAHFMVVTLFFGPCIFLYTRPDSSFSIDKVVSVFYTVVTP 280


RESULT 7
US-09-886-055-309
; Sequence 309, Application US/09886055
; Patent No. US20020132273A1
; GENERAL INFORMATION:
;  APPLICANT: STRYER, LUBERT
;  APPLICANT:  ZOZULYA, SERGEY
;  TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND
;  TITLE OF INVENTION:  BIOSENSORS OF CHEMICAL SENSANTS
;  FILE REFERENCE: 078003-0277150
;  CURRENT APPLICATION NUMBER: US/09/886,055
;  CURRENT FILING DATE:  2001-06-22
;  PRIOR APPLICATION NUMBER: 60/213,812
;  PRIOR FILING DATE: 2000-06-22
;  NUMBER OF SEQ ID NOS: 522
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 309
;   LENGTH: 311
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-886-055-309

  Query Match             58.2%;  Score 938;  DB 10;  Length 311;
  Best Local Similarity   55.4%;  Pred. No. 4.5e-83;
  Matches  170;  Conservative   59;  Mismatches   76;  Indels    2;  Gaps    1;

Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              |: :|   ||||:| ||: :  :| : |: ||  |:: | ||:||::    :    :|||
Db          1 MEKIN--NVTEFIFWGLSQSPEIEKVCFVVFSFFYIIILLGNLLIMLTVCLSNLFKSPMY 58

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
              |||| |||:|||:|||| |||:  || : ||||:  |: ||  :| | | |||:| ::||
Db         59 FFLSFLSFVDICYSSVTAPKMIVDLLAKDKTISYVGCMLQLLGVHFFGCTEIFILTVMAY 118

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
              ||||||| ||||  :||   | :::   |:|| :||: |  | ::||:|||| || ||||
Db        119 DRYVAICKPLHYMTIMNRETCNKMLLGTWVGGFLHSIIQVALVVQLPFCGPNEIDHYFCD 178

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTC 240
              |  |:|||||:||: |:::  |||||:|  |: :: || :|||||| |||||:||||||
Db        179 VHPVLKLACTETYIVGVVVTANSGTIALGSFVILLISYSIILVSLRKQSAEGRRKALSTC 238

Qy        241 SAHFMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300
               :|  :| :||||| |:| ||||:|| ||:|:||||::||:||| |||||| |||:|||:
Db        239 GSHIAMVVIFFGPCTFMYMRPDTTFSEDKMVAVFYTIITPMLNPLIYTLRNAEVKNAMKK 298

Qy        301 LRQRQVF 307
              |  | ||
Db        299 LWGRNVF 305


RESULT 8
US-09-804-291-309
; Sequence 309, Application US/09804291
; Publication No. US20030088059A1
; GENERAL INFORMATION:
;  APPLICANT: ZOZULA, SERGEY
;  TITLE OF INVENTION: HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME
;  FILE REFERENCE: P 0278005
```

```
;  CURRENT APPLICATION NUMBER: US/09/804,291
;  CURRENT FILING DATE:  2001-03-13
;  PRIOR APPLICATION NUMBER: 60/188,914
;  PRIOR FILING DATE: 2000-03-13
;  PRIOR APPLICATION NUMBER: 60/192,033
;  PRIOR FILING DATE: 2000-03-24
;  PRIOR APPLICATION NUMBER: 60/198,474
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: 60/199,335
;  PRIOR FILING DATE: 2000-04-24
;  PRIOR APPLICATION NUMBER: 60/207,702
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 60/213,849
;  PRIOR FILING DATE: 2000-06-23
;  PRIOR APPLICATION NUMBER: 60/226,534
;  PRIOR FILING DATE: 2000-08-16
;  PRIOR APPLICATION NUMBER: 60/230,732
;  PRIOR FILING DATE: 2000-09-07
;  PRIOR APPLICATION NUMBER: 60/266,862
;  PRIOR FILING DATE: 2001-02-07
;  NUMBER OF SEQ ID NOS: 529
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 309
;   LENGTH: 311
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-804-291-309

  Query Match             58.2%;  Score 938;  DB 11;  Length 311;
  Best Local Similarity   55.4%;  Pred. No. 4.5e-83;
  Matches  170;  Conservative   59;  Mismatches   76;  Indels    2;  Gaps    1;

Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              |: :|   ||||:| ||: :  :| : |: ||  |:: | ||:||::    :    :|||
Db          1 MEKIN--NVTEFIFWGLSQSPEIEKVCFVVFSFFYIIILLGNLLIMLTVCLSNLFKSPMY 58

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
              |||| |||:|||:|||| |||:  || : ||||:  |: ||  :| | | |||:| ::||
Db         59 FFLSFLSFVDICYSSVTAPKMIVDLLAKDKTISYVGCMLQLLGVHFFGCTEIFILTVMAY 118

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
              ||||||| ||||  :||   | :::   |:|| :||: |  | ::||:|||| || ||||
Db        119 DRYVAICKPLHYMTIMNRETCNKMLLGTWVGGFLHSIIQVALVVQLPFCGPNEIDHYFCD 178

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTC 240
              |  |:|||||:||: |:::  |||||:|  |: :: || :|||||| |||||:||||||
Db        179 VHPVLKLACTETYIVGVVVTANSGTIALGSFVILLISYSIILVSLRKQSAEGRRKALSTC 238

Qy        241 SAHFMVVALPFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300
              :|  :| :||||| |:| ||||:|| ||:|:||||::||:||| |||||| |||:|||:
Db        239 GSHIAMVVIFFGPCTFMYMRPDTTFSEDKMVAVFYTIITPMLNPLIYTLRNAEVKNAMKK 298

Qy        301 LRQRQVF 307
              |  | ||
Db        299 LWGRNVF 305


RESULT 9
US-09-886-055-403
; Sequence 403, Application US/09886055
; Patent No. US20020132273A1
; GENERAL INFORMATION:
;  APPLICANT: STRYER, LUBERT
;  APPLICANT:  ZOZULYA, SERGEY
;  TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND
;  TITLE OF INVENTION:  BIOSENSORS OF CHEMICAL SENSANTS
;  FILE REFERENCE: 078003-0277150
;  CURRENT APPLICATION NUMBER: US/09/886,055
;  CURRENT FILING DATE:  2001-06-22
;  PRIOR APPLICATION NUMBER: 60/213,812
;  PRIOR FILING DATE: 2000-06-22
;  NUMBER OF SEQ ID NOS: 522
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 403
;   LENGTH: 314
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-886-055-403

  Query Match             57.7%;  Score 929;  DB 10;  Length 314;
  Best Local Similarity   53.1%;  Pred. No. 3.4e-82;
  Matches  165;  Conservative   67;  Mismatches   79;  Indels    0;  Gaps    0;

Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              ||  |:: ::||| |||::  |:| ||| || :|: |: || ||:|  :  | ||:|||
Db          1 MDVGNKSTMSEFVLLGLSNSWELQMFFFMVFSLLYVATMVGNSLIVITVIVDPHLHSPMY 60

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
              | |:||| ||:  :|   |||:   |   |||||| |:||:|||||   || ||: :::
Db         61 FLLTNLSIIDMSLASFATPKMITDYLTGHKTISFDGCLTQIFFLHLFTGTEIILLMAMSF 120

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
              |||:||| |||| :|:: :||: || | |: | :||: |     : ||:|||  :||:|||
Db        121 DRYIAICKPLHYASVISPQVCVALVVASWIMGVMHSMSQVIFALTLPFCGPYEVDSFFCD 180

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTC 240
              :|:| :||| |||: |: ::: || |:||||: :  ||:::||::: ||: |  ||||||
Db        181 LPVVFQLACVDTYVLGLFMISTSGIIALSCFIVLFNSYVIVLVTVKHHSSRGSSKALSTC 240

Qy        241 SAHFMVVALPFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300
              :|||:|| ||||||||||  | :||  ||::|||||: || ||| |||||:||| ||::
Db        241 TAHPIVVFLPFGPCIFIYMWPLSSFLTDKILSVFYTIFTPTLNPIIYTLRNQEVKIAMRK 300

Qy        301 LRQRQVFFTKS 311
              |: | : | |:
Db        301 LKNRFLNFNKA 311


RESULT 10
US-09-804-291-403
; Sequence 403, Application US/09804291
; Publication No. US20030088059A1
; GENERAL INFORMATION:
;  APPLICANT: ZOZULA, SERGEY
;  TITLE OF INVENTION: HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME
;  FILE REFERENCE: P 0278005
;  CURRENT APPLICATION NUMBER: US/09/804,291
;  CURRENT FILING DATE:  2001-03-13
;  PRIOR APPLICATION NUMBER: 60/188,914
;  PRIOR FILING DATE: 2000-03-13
;  PRIOR APPLICATION NUMBER: 60/192,033
;  PRIOR FILING DATE: 2000-03-24
;  PRIOR APPLICATION NUMBER: 60/198,474
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: 60/199,335
;  PRIOR FILING DATE: 2000-04-24
;  PRIOR APPLICATION NUMBER: 60/207,702
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 60/213,849
;  PRIOR FILING DATE: 2000-06-23
;  PRIOR APPLICATION NUMBER: 60/226,534
;  PRIOR FILING DATE: 2000-08-16
;  PRIOR APPLICATION NUMBER: 60/230,732
;  PRIOR FILING DATE: 2000-09-07
;  PRIOR APPLICATION NUMBER: 60/266,862
;  PRIOR FILING DATE: 2001-02-07
;  NUMBER OF SEQ ID NOS: 529
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 403
;   LENGTH: 314
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-804-291-403

  Query Match             57.7%;  Score 929;  DB 11;  Length 314;
  Best Local Similarity   53.1%;  Pred. No. 3.4e-82;
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  Matches  165;  Conservative   67;  Mismatches   79;  Indels    0;  Gaps    0;

Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              ||  |:: ::||| |||:::  |:| ||| || :|: |: || ||:|  :  | ||:|||
Db          1 MDVGNKSTMSEFVLLGLSNSWELQMFFFMVFSLLYVATMVGNSLIVITVIVDPHLHSPMY 60

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
              | |:||| ||:  :|   |||:   |   |||||| |:||:|||||   || ||: :::
Db         61 FLLTNLSIIDMSLASFATPKMITDYLTGHKTISFDGCLTQIFFLHLFTGTEIILLMAMSF 120

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
              |||:||| |||| :|:: :||: || | |: | :||: |    : ||:|||  :||:|||
Db        121 DRYIAICKPLHYASVISPQVCVALVVASWIMGVMHSMSQVIFALTLPFCGPYEVDSFFCD 180

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTC 240
              :|:| :||| |||: |: ::: || |:|||: :  ||:::||::: ||: |  ||||||
Db        181 LPVVFQLACVDTYVLGLFMISTSGIIALSCFIVLFNSYVIVLVTVKHHSSRGSSKALSTC 240

Qy        241 SAHFMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300
              :|||:|| |||||||||| | :||  ||::|||||: || ||| ||||||:||| ||::
Db        241 TAHFIVVFLFFGPCIFIYMWPLSSFLTDKILSVFYTIFTPTLNPIIYTLRNQEVKIAMRK 300

Qy        301 LRQRQVFFTKS 311
              |: | : | |:
Db        301 LKNRFLNFNKA 311


RESULT 11
US-10-017-161-402
; Sequence 402, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
;  APPLICANT: SUWA, MAKIKO
;  APPLICANT:  ASAI, KIYOSHI
;  APPLICANT:  AKIYAMA, YUTAKA
;  APPLICANT:  ABURATANI, HIROYUKI
;  TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
;  FILE REFERENCE: 084335/0152
;  CURRENT APPLICATION NUMBER: US/10/017,161
;  CURRENT FILING DATE:  2002-12-18
;  PRIOR APPLICATION NUMBER: JP 2001/246789
;  PRIOR FILING DATE: 2001-06-18
;  NUMBER OF SEQ ID NOS: 2430
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 402
;   LENGTH: 314
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-017-161-402

  Query Match           57.7%;  Score 929;  DB 12;  Length 314;
  Best Local Similarity   53.1%;  Pred. No. 3.4e-82;
  Matches  165;  Conservative   67;  Mismatches   79;  Indels    0;  Gaps    0;

Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              ||  |:: ::||| |||:::  |:| ||| || :|: |: || ||:|  :  | ||:|||
Db          1 MDVGNKSTMSEFVLLGLSNSWELQMFFFMVFSLLYVATMVGNSLIVITVIVDPHLHSPMY 60

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
              | |:||| ||:  :|   |||:   |   |||||| |:||:|||||   || ||: :::
Db         61 FLLTNLSIIDMSLASFATPKMITDYLTGHKTISFDGCLTQIFFLHLFTGTEIILLMAMSF 120

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
              |||:||| |||| :|:: :||: || | |: | :||: |    : ||:|||  :||:|||
Db        121 DRYIAICKPLHYASVISPQVCVALVVASWIMGVMHSMSQVIFALTLPFCGPYEVDSFFCD 180

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTC 240
              :|:| :||| |||: |: ::: || |:|||: :  ||:::||::: ||: |  ||||||
Db        181 LPVVFQLACVDTYVLGLFMISTSGIIALSCFIVLFNSYVIVLVTVKHHSSRGSSKALSTC 240

Qy        241 SAHFMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300
              :|||:|| |||||||||| | :||  ||::|||||: || ||| ||||||:||| ||::
Db        241 TAHFIVVFLFFGPCIFIYMWPLSSFLTDKILSVFYTIFTPTLNPIIYTLRNQEVKIAMRK 300

Qy        301 LRQRQVFFTKS 311
              |: | : | |:
Db        301 LKNRFLNFNKA 311


RESULT 12
US-09-886-055-447
; Sequence 447, Application US/09886055
; Patent No. US20020132273A1
; GENERAL INFORMATION:
;  APPLICANT: STRYER, LUBERT
;  APPLICANT:  ZOZULYA, SERGEY
;  TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND
;  TITLE OF INVENTION:  BIOSENSORS OF CHEMICAL SENSANTS
;  FILE REFERENCE: 078003-0277150
;  CURRENT APPLICATION NUMBER: US/09/886,055
;  CURRENT FILING DATE:  2001-06-22
;  PRIOR APPLICATION NUMBER: 60/213,812
;  PRIOR FILING DATE: 2000-06-22
;  NUMBER OF SEQ ID NOS: 522
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 447
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-886-055-447

  Query Match           57.6%;  Score 927.5;  DB 10;  Length 310;
  Best Local Similarity   55.0%;  Pred. No. 4.7e-82;
  Matches  170;  Conservative   60;  Mismatches   78;  Indels    1;  Gaps    1;

Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLH-TPM 59
              ||  | : |:|||  ||  :| |:  ||: |  :|:  : ||:||::  :  | || :||
Db          1 MDPQNYSLVSEFVLHGLCTSRHLQNFFFIFFPGVYVAIMLGNLLILVTVISDPCLHSSPM 60

Qy         60 YFFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVA 119
              || | ||:|:|:  :|   |||:   | ::| |||  |: |:|||    ||: ||: :|
Db         61 YFLLGNLAFLDMWLASFATPKMIRDFLSDQKLISFGGCMAQIFFLHFTGGAEMVLLVSMA 120

Qy        120 YDRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFC 179
              |||||||| ||||  :|: : ||:|| | |: | |||: |   |: |||||| :||:||
Db        121 YDRYVAICKPLHYMTLMSWQTCIRLVLASWVVGFVHSISQVAFTVNLPYCGPNEVDSFFC 180

Qy        180 DVPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALST 239
              |:|||||||| |||: ||:::::|| :|||||| :: || |||:::|: :|     |||||
Db        181 DLPLVIKLACMDTYVLGIIMISDSGLLSLSCFLLLLISYTVILLAIRQRAAGSTSKALST 240

Qy        240 CSAHFMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMK 299
              |||| ||| |||||||:| || : ||:||::|||||: |||||| ||||||||:|:|||
Db        241 CSAHIMVVTLFFGPCIFVYVRPFSRFSVDKLLSVFYTIFTPLLNPIIYTLRNEEMKAAMK 300

Qy        300 QLRQRQVFF 308
              :|: |:| |
Db        301 KLQNRRVTF 309


RESULT 13
US-09-804-291-447
; Sequence 447, Application US/09804291
; Publication No. US20030088059A1
; GENERAL INFORMATION:
;  APPLICANT: ZOZULA, SERGEY
;  TITLE OF INVENTION: HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME
;  FILE REFERENCE: P 0278005
;  CURRENT APPLICATION NUMBER: US/09/804,291
;  CURRENT FILING DATE:  2001-03-13
;  PRIOR APPLICATION NUMBER: 60/188,914
;  PRIOR FILING DATE: 2000-03-13
;  PRIOR APPLICATION NUMBER: 60/192,033
;  PRIOR FILING DATE: 2000-03-24
;  PRIOR APPLICATION NUMBER: 60/198,474
;  PRIOR FILING DATE: 2000-04-14
```

```
;  PRIOR APPLICATION NUMBER: 60/199,335
;  PRIOR FILING DATE: 2000-04-24
;  PRIOR APPLICATION NUMBER: 60/207,702
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 60/213,849
;  PRIOR FILING DATE: 2000-06-23
;  PRIOR APPLICATION NUMBER: 60/226,534
;  PRIOR FILING DATE: 2000-08-16
;  PRIOR APPLICATION NUMBER: 60/230,732
;  PRIOR FILING DATE: 2000-09-07
;  PRIOR APPLICATION NUMBER: 60/266,862
;  PRIOR FILING DATE: 2001-02-07
;  NUMBER OF SEQ ID NOS: 529
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 447
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-804-291-447

  Query Match             57.6%;  Score 927.5;  DB 11;  Length 310;
  Best Local Similarity   55.0%;  Pred. No. 4.7e-82;
  Matches  170;  Conservative   60;  Mismatches   78;  Indels    1;  Gaps    1;

Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLH-TPM 59
              ||  | : |:|||  ||  :| |:  ||: |  :|:  : ||:||:: |  :  | || :||
Db          1 MDPQNYSLVSEFVLHGLCTSRHLQNFFFIFFFGVYVAIMLGNLLILVTVISDPCLHSSPM 60

Qy         60 YFFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVA 119
              || | ||:|:|:  :|   |||:   | ::| |||  |: |:||||    ||: ||: :|
Db         61 YFLLGNLAFLDMWLASFATPKMIRDFLSDQKLISFGGCMAQIFFLHFTGGAEMVLLVSMA 120

Qy        120 YDRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFC 179
              |||||||| ||||  :|: : ||:|| | |: | |||: |    |: |||||| :||:||
Db        121 YDRYVAICKPLHYMTLMSWQTCIRLVLASWVVGFVHSISQVAFTVNLPYCGPNEVDSFFC 180

Qy        180 DVPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALST 239
              |:|||||||| |||: ||:::::|| :|||||  :: || |||:::|: :|    |||||
Db        181 DLPLVIKLACMDTYVLGIIMISDSGLLSLSCFLLLLISYTVILLAIRQRAAGSTSKALST 240

Qy        240 CSAHFMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMK 299
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RESULT 14
US-10-023-601-34
; Sequence 34, Application US/10023601
; Publication No. US20030083463A1
; GENERAL INFORMATION:
;  APPLICANT: Padigaru, Muralidhara
;  APPLICANT:  Kekuda, Ramesh
;  APPLICANT:  Colman, Steven
;  APPLICANT:  Spytek, Kimberly
;  APPLICANT:  Ballinger, Robert
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  Li, Li
;  APPLICANT:  Shenoy, Suresh
;  APPLICANT:  Casman, Stacie
;  APPLICANT:  Guzev, Vladimir
;  TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 21402-224AF
;  CURRENT APPLICATION NUMBER: US/10/023,601
;  CURRENT FILING DATE:  2001-12-18
;  PRIOR APPLICATION NUMBER: 60/256,635
;  PRIOR FILING DATE: 2000-12-18
;  PRIOR APPLICATION NUMBER: 60/259,743
;  PRIOR FILING DATE: 2001-01-04
;  PRIOR APPLICATION NUMBER: 60/299,327
;  PRIOR FILING DATE: 2001-06-19
;  PRIOR APPLICATION NUMBER: 60/261,498
;  PRIOR FILING DATE: 2001-01-12
;  PRIOR APPLICATION NUMBER: 60/263,689
;  PRIOR FILING DATE: 2001-01-24
;  PRIOR APPLICATION NUMBER: 60/267,464
;  PRIOR FILING DATE: 2001-02-08
;  PRIOR APPLICATION NUMBER: 60/271,021
;  PRIOR FILING DATE: 2001-02-22
;  PRIOR APPLICATION NUMBER: 60/275,946
;  PRIOR FILING DATE: 2001-03-14
;  PRIOR APPLICATION NUMBER: 60/278,150
;  PRIOR FILING DATE: 2001-03-23
;  PRIOR APPLICATION NUMBER: 60/285,718
;  PRIOR FILING DATE: 2001-04-23
;  PRIOR APPLICATION NUMBER: 60/312,902
;  PRIOR FILING DATE: 2001-08-16
;  PRIOR APPLICATION NUMBER: 60/257,876
;  PRIOR FILING DATE: 2000-12-21
;  PRIOR APPLICATION NUMBER: 60/260,718
;  PRIOR FILING DATE: 2001-01-10
;  PRIOR APPLICATION NUMBER: 60/284,591
;  PRIOR FILING DATE: 2001-04-18
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
;   LENGTH: 324
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-023-601-34

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  Best Local Similarity   56.2%;  Pred. No. 3.3e-81;
  Matches  171;  Conservative   50;  Mismatches   83;  Indels    0;  Gaps    0;

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Db          1 MNETNHSRVTEFVLLGLSSSRELQPFLFLTFSLLYLAILLGNFLIILTVTSDSRLHTPMY 60

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
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Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
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Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTC 240
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Db        181 LPLVTKLACIDTYVVSLLIVADSGFLSLSSFLLLVVSYTVILVTVRNRSSASMAKARSTL 240

Qy        241 SAHFMVVALFFGPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300
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RESULT 15
US-09-886-055-409
; Sequence 409, Application US/09886055
; Patent No. US20020132273A1
; GENERAL INFORMATION:
;  APPLICANT: STRYER, LUBERT
;  APPLICANT:  ZOZULYA, SERGEY
;  TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND
;  TITLE OF INVENTION:  BIOSENSORS OF CHEMICAL SENSANTS
;  FILE REFERENCE: 078003-0277150
;  CURRENT APPLICATION NUMBER: US/09/886,055
;  CURRENT FILING DATE:  2001-06-22
;  PRIOR APPLICATION NUMBER: 60/213,812
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;  PRIOR FILING DATE: 2000-06-22
;  NUMBER OF SEQ ID NOS: 522
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 409
;   LENGTH: 348
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-886-055-409

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  Best Local Similarity   56.2%;  Pred. No. 3.6e-81;
  Matches  171;  Conservative   50;  Mismatches   83;  Indels    0;  Gaps    0;

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Qy         61 PFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
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Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
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Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTC 240
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Db        265 TAHITVVTLFFGPCIFIYVWPFSSYSVDKVLAVFYTIFTLILNPVIYTLRNKEVKAAMSK 324

Qy        301 LRQR 304
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Db        325 LKSR 328


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Job time : 25 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 12, 2003, 16:05:31 ; Search time 30 Seconds
(without alignments)
441.443 Million cell updates/sec

Title: US-09-807-132-4
Perfect score: 1611
Sequence: 1 MDSLNQTRVTEFVFLGLTDN.....VKSAMKQLRQRQVFFTKSYT 313

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	674.5	41.9	333	3	US-08-988-876-6	Sequence 6, Appli
2	667.5	41.4	309	3	US-08-988-876-5	Sequence 5, Appli
3	656	40.7	314	3	US-08-988-876-7	Sequence 7, Appli
4	640	39.7	313	4	US-09-465-901-48	Sequence 48, Appl
5	639.5	39.7	321	3	US-08-748-506-18	Sequence 18, Appl
6	634.5	39.4	321	3	US-08-748-506-10	Sequence 10, Appl
7	628.5	39.0	321	3	US-08-748-506-20	Sequence 20, Appl
8	626.5	38.9	321	3	US-08-748-506-19	Sequence 19, Appl
9	623.5	38.7	321	3	US-08-748-506-11	Sequence 11, Appl
10	623.5	38.7	321	3	US-08-748-506-12	Sequence 12, Appl
11	617.5	38.3	321	3	US-08-748-506-13	Sequence 13, Appl
12	599.5	37.2	284	1	US-08-118-270-61	Sequence 61, Appl
13	599.5	37.2	284	5	PCT-US93-08528-61	Sequence 61, Appl
14	573	35.6	293	1	US-08-118-270-60	Sequence 60, Appl
15	573	35.6	293	5	PCT-US93-08528-60	Sequence 60, Appl
16	567	35.2	284	1	US-08-118-270-67	Sequence 67, Appl
17	567	35.2	284	5	PCT-US93-08528-67	Sequence 67, Appl
18	560.5	34.8	316	2	US-08-827-291A-2	Sequence 2, Appli
19	553.5	34.4	286	1	US-08-118-270-65	Sequence 65, Appl
20	553.5	34.4	286	5	PCT-US93-08528-65	Sequence 65, Appl
21	553.5	34.4	327	3	US-08-748-506-24	Sequence 24, Appl
22	551.5	34.2	327	3	US-08-748-506-14	Sequence 14, Appl
23	541	33.6	296	2	US-08-467-948A-2	Sequence 2, Appli
24	541	33.6	296	3	US-08-467-947A-2	Sequence 2, Appli
25	540.5	33.6	275	1	US-08-118-270-66	Sequence 66, Appl
26	540.5	33.6	275	5	PCT-US93-08528-66	Sequence 66, Appl
27	540.5	33.6	327	3	US-08-748-506-22	Sequence 22, Appl
28	540.5	33.6	327	3	US-08-748-506-23	Sequence 23, Appl
29	537	33.3	277	1	US-08-118-270-68	Sequence 68, Appl
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38	518.5	32.2	247	5	PCT-US95-07093-3	Sequence 3, Appli
39	516.5	32.1	277	1	US-08-118-270-62	Sequence 62, Appl
40	516.5	32.1	277	5	PCT-US93-08528-62	Sequence 62, Appl
41	485.5	30.1	223	4	US-09-465-901-38	Sequence 38, Appl
42	475.5	29.5	273	1	US-08-118-270-63	Sequence 63, Appl
43	475.5	29.5	273	5	PCT-US93-08528-63	Sequence 63, Appl
44	473	29.4	222	4	US-09-465-901-44	Sequence 44, Appl
45	469.5	29.1	223	4	US-09-465-901-20	Sequence 20, Appl

ALIGNMENTS

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RESULT 1
US-08-988-876-6
; Sequence 6, Application US/08988876
; Patent No. 6063596
;  GENERAL INFORMATION:
;    APPLICANT:  Lal, Preeti
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Hillman, Jennifer L.
;    APPLICANT:  Yue, Henry
;    TITLE OF INVENTION:  G PROTEIN COUPLED RECEPTORS ASSOCIATED
;    TITLE OF INVENTION:  WITH IMMUNE RESPONSE
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/988,876
;      FILING DATE:  Herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0441 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-855-0555
;      TELEFAX:  650-845-4166
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  333 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GenBank
;      CLONE:  205814
US-08-988-876-6
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  Best Local Similarity   43.9%;  Pred. No. 1.5e-49;
  Matches  133;  Conservative   62;  Mismatches  105;  Indels    3;  Gaps    2;

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Db          1 MDSSNRTRVSEFLLLGFVENKDLQPLIYGLFLSMYLVTVIGNISIIVAIISDPCLHTPMY 60

Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
              |||||||||:|||  | ||||||  :  :   |::  ||||::|  ||   : ||| |:||
Db         61 FFLSNLSFVDICFISTTVPKMLVNIQTQNNVITYAGCITQIYFFLLFVELDNFLLTIMAY 120

Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
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Db        121 DRYVAICHPMHYTVIMNYKLCGFLVLVSWIVSVLHALFQSLMMLALPFCTHLEIPHYFCE 180

Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSL-RKHSAEGRQKALST 239
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Db        181 PNQVIQLTCSDAFLNDLVIYFTLVLLATVPLAGIFYSYFKIVSSICAISSVHGKYKAFST 240

Qy        240 CSAHFMVVALFF--GPCIFIYTRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSA 297
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Db        241 CASHLSVVSLFYCTGLGVYLSSAANNSSQASATASVMYTVVTPMVNPFIYSLRNKDVKSV 300

Qy        298 MKQ 300
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Db        301 LKK 303


RESULT 2
US-08-988-876-5
; Sequence 5, Application US/08988876
; Patent No. 6063596
;  GENERAL INFORMATION:
;    APPLICANT:  Lal, Preeti
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Hillman, Jennifer L.
;    APPLICANT:  Yue, Henry
;    TITLE OF INVENTION:  G PROTEIN COUPLED RECEPTORS ASSOCIATED
;    TITLE OF INVENTION:  WITH IMMUNE RESPONSE
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/988,876
;      FILING DATE:  Herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0441 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-855-0555
;      TELEFAX:  650-845-4166
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  309 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GenBank
;      CLONE:  1314667
US-08-988-876-5

  Query Match             41.4%;  Score 667.5;  DB 3;  Length 309;
  Best Local Similarity   41.8%;  Pred. No. 5.4e-49;
  Matches  130;  Conservative   71;  Mismatches  101;  Indels    9;  Gaps    3;

Qy          1 MDSLNQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMY 60
              |:  | ||: ||: || ::   |:   |  | ::|::|: ||:|:|:|      ||||||
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Qy         61 FFLSNLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAY 120
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Qy        121 DRYVAICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCD 180
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Qy        181 VPLVIKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRK-HSAEGRQKALST 239
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Db        181 LNQMIQLACSDTFLNNMMLYFAAILLGVAPLVGVLYSYFKIVSSIRGISSAHSKYKAFST 240

Qy        240 CSAHFMVVALFFGPCIFIY--TRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSA 297
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Db        241 CASHLSVVSLFYCTSLGVYLSSAAPQSTHTSSVASVMYTVVTPMLNPFIYSLRNKDIKGA 300

Qy        298 MKQLRQRQVFF 308
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RESULT 3
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; Sequence 7, Application US/08988876
; Patent No. 6063596
;  GENERAL INFORMATION:
;    APPLICANT:  Lal, Preeti
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Hillman, Jennifer L.
;    APPLICANT:  Yue, Henry
;    TITLE OF INVENTION:  G PROTEIN COUPLED RECEPTORS ASSOCIATED
;    TITLE OF INVENTION:  WITH IMMUNE RESPONSE
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/988,876
;      FILING DATE:  Herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0441 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-855-0555
;      TELEFAX:  650-845-4166
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;       TELEX:
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;       LENGTH:  314 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;       LIBRARY:  GenBank
;       CLONE:  32086
US-08-988-876-7

  Query Match             40.7%;  Score 656;  DB 3;  Length 314;
  Best Local Similarity   43.4%;  Pred. No. 5.1e-48;
  Matches  134;  Conservative   67;  Mismatches  104;  Indels    4;  Gaps    3;

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Db          5 NQTSISDFLLLGLPIQPEQQNLCYALFLAMYLTTLLGNLLIIVLIRLDSHLHTPMYLFLS 64

Qy         65 NLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAYDRYV 124
              |||| |:| ||||:||:|: :  :  :| : :|:||::|  ||   |||||: :||||||
Db         65 NLSFSDLCFSSVTIPKLLQNMQNQDPSIPYADCLTQMYFFLLFGDLESFLLVAMAYDRYV 124

Qy        125 AICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCDVPLV 184
              ||| |||| :|:  :|: ||    |:  | |::  | |  || :|  |:|  :|||:  :
Db        125 AICFPLHYTAIMSPMLCLALVALSWVLTTFHAMLHTLLMARLCFCADNVIPHFFCDMSAL 184

Qy        185 IKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVSLRK-HSAEGRQKALSTCSAH 243
              :||| :|| :   :|    | | :  || :: ||  |: |: |  |::|  || ||| :|
Db        185 LKLAFSDTRVNEWVIFIMGGLILVIPFLLILGSYARIVSSILKVPSSKGICKAFSTCGSH 244

Qy        244 FMVVALFFGPCIFIY--TRPDTSFSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ- 300
                ||:||:|  | :|  :  ::|    | |::: ||||||:||||||:||| ::| |: :
Db        245 LSVVSLFYGTVIGLYLCSSANSSTLKDTVMAMMYTVVTPMLNPFIYSLRNRDMKGALSRV 304

Qy        301 LRQRQVFFT 309
              : |:: ||:
Db        305 IHQKKTFFS 313


RESULT 4
US-09-465-901-48
; Sequence 48, Application US/09465901
; Patent No. 6492143
; GENERAL INFORMATION:
;  APPLICANT: Reed, Randall
;  APPLICANT:  Yau, King-Wai
;  APPLICANT:  Krautwurst, Dietmar
;  TITLE OF INVENTION: Olfactory Receptor Expession Libraries
;  TITLE OF INVENTION:  ad Methods of Making and Using Them
;  FILE REFERENCE: 001107.00105
;  CURRENT APPLICATION NUMBER: US/09/465,901
;  CURRENT FILING DATE:  2001-12-17
;  PRIOR APPLICATION NUMBER: 60/112,605
;  PRIOR FILING DATE: 1998-12-17
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
;   LENGTH: 313
;   TYPE: PRT
;   ORGANISM: Mus musculus
;   FEATURE:
;   OTHER INFORMATION: PCR primer
US-09-465-901-48

  Query Match             39.7%;  Score 640;  DB 4;  Length 313;
  Best Local Similarity   44.9%;  Pred. No. 1.1e-46;
  Matches  136;  Conservative   51;  Mismatches  106;  Indels   10;  Gaps    5;

Qy          5 NQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMYFFLS 64
              | | ||||: |||:|   |::| |: |   | | | || |||  |:    |:||||:||
Db          3 NSTTVTEFILLGLSDACELQVLIFLGFLLTYFLILLGNFLIIFITLVDRRLYTPMYYFLR 62

Qy         65 NLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAYDRYV 124
              | : ::|  :||  |||  ::   ||||   |  | |         | ||| ::::||||
Db         63 NFAMLEIWFTSVIFPKMLTNIITGHKTISLLGCFLQAFLYFFLGTTEFPLLAVMSFDRYV 122

Qy        125 AICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCDVPLV 184
              ||| || |  :|: |||:||||  |: | :  :  : :  : |:||||||: :|||   :
Db        123 AICNPLRYATIMSKRVCVQLVFCSWMSGLLLIIVPSSIVFQQPFCGPNIINHFFCDNFPL 182

Qy        185 IKLACTDTYLTGIL--IVTNSGTISLSCFLAV-VTSYMVILVS-LRKHSAEGRQKALSTC 240
              ::| | || |   |  :: |    ||   ||| | |  || : |   ||: |:|| |||
Db        183 MELICADTSLVEFLGFVIAN---FSLLGTLAVTATCYGHILYTILHIPSAKERKKAFSTC 239

Qy        241 SAHFMVVALFFGPCIFIYTRPDTS---FSIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSA 297
              |:| :||:||:| |||:| |   :      :|||::  ||||| ||||||||||::||
Db        240 SSHIIVVSLFYGSCIFMYVRSGKNGQGEDHNKVVALLNTVVTPTLNPFIYTLRNKQVKQV 299

Qy        298 MKQ 300
              ::
Db        300 FRE 302


RESULT 5
US-08-748-506-18
; Sequence 18, Application US/08748506
; Patent No. 6159707
;  GENERAL INFORMATION:
;    APPLICANT:  Ronnett et al.
;    TITLE OF INVENTION:  NOVEL SPERM RECEPTORS
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Leydig, Voit & Mayer, Ltd.
;      STREET:  Two Prudential Plaza, Suite 4900
;      CITY:  Chicago
;      STATE:  IL
;      COUNTRY:  US
;      ZIP:  60601-6780
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/748,506
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/033,751
;      FILING DATE:  09-NOV-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      REFERENCE/DOCKET NUMBER:  74940
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-616-5600
;      TELEFAX:  312-616-5700
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  321 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
US-08-748-506-18

  Query Match             39.7%;  Score 639.5;  DB 3;  Length 321;
  Best Local Similarity   43.1%;  Pred. No. 1.3e-46;
  Matches  132;  Conservative   58;  Mismatches   99;  Indels   17;  Gaps    4;

Qy          5 NQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMYFFLS 64
              |   | | |  ::      | |     :::::|:|||||::|   :|||||||||:
Db         11 NSLTVKHFAFAKFSEVPGECFLLFNLILLMFLVSLTGNILIVLAICTSPSLHTPMYFFLA 70

Qy         65 NLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAYDRYV 124
              ||| ::| ::   :||||: |: | : || : | ||:||   |   |  ||  :|:|| :
```

```
Db         71 NLSLLEIGYTCSVIPKMLQSLVSEAREISREGCATQMFFFAFFGITECCLLAAMAFDRCM 130

Qy        125 AICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCDVPLV 184
              |||:||||   |:  ||  |    |  | : |||||     | :|||  || :|||:| :
Db        131 AICSPLHYATRMSREVCAHLAIVSWGMGCIVSLGQTNFIFSLNFCGPCEIDHFFCDLPPL 190

Qy        185 IKLACTDT-------YLTGILIVTNSGTISLSCFLAVVTSYMVILVS-LRKHSAEGRQKA 236
              : ||| ||       ::  :| ::       | || :: ||: ||:: |   | ||| ||
Db        191 LALACGDTSQNEAAIFVVAVLCIS-------SPFLLIIYSYVKILIAVLLMPSPEGRHKA 243

Qy        237 LSTCSAHFMVVALFFGPCIFIYTRPDTSFS--IDKVVSVFYTVVTPLLNPFIYTLRNEEV 294
              |||||:| :|| ||:|     | || :| |  :|| :::|||||| :||| ||:|||:||
Db        244 LSTCSSHLLVVTLFYGSACITYLRPKSSHSPGMDKFLALFYTVVTSMLNPIIYSLRNKEV 303

Qy        295 KSAMKQ 300
              |:|:::
Db        304 KAALRR 309


RESULT 6
US-08-748-506-10
; Sequence 10, Application US/08748506
; Patent No. 6159707
;  GENERAL INFORMATION:
;    APPLICANT:  Ronnett et al.
;    TITLE OF INVENTION:  NOVEL SPERM RECEPTORS
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Leydig, Voit & Mayer, Ltd.
;      STREET:  Two Prudential Plaza, Suite 4900
;      CITY:  Chicago
;      STATE:  IL
;      COUNTRY:  US
;      ZIP:  60601-6780
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/748,506
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/033,751
;      FILING DATE:  09-NOV-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      REFERENCE/DOCKET NUMBER:  74940
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-616-5600
;      TELEFAX:  312-616-5700
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  321 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-748-506-10

  Query Match             39.4%;  Score 634.5;  DB 3;  Length 321;
  Best Local Similarity   42.8%;  Pred. No. 3.4e-46;
  Matches  131;  Conservative   58;  Mismatches  100;  Indels   17;  Gaps    4;

Qy          5 NQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMYFFLS 64
              |   |  | |   ::      | |     :::::|:|| ||::|   :||||||||||:
Db         11 NSLTVKHFAFAKFSEVPGECFLLFNLILLMFLVSLTGNTLIVLAICTSPSLHTPMYFFLA 70

Qy         65 NLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAYDRYV 124
              ||| ::| ::   :||||: |: | : || : | ||:||   |   |  ||  :|:|| :
Db         71 NLSLLEIGYTCSVIPKMLQSLVSEAREISREGCATQMFFFAFFGITECCLLAAMAFDRCM 130

Qy        125 AICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCDVPLV 184
              |||:||||   |:  ||  |    |  | : |||||     | :|||  || :|||:| :
Db        131 AICSPLHYATRMSREVCAHLAIVSWGMGCIVSLGQTNFIFSLNFCGPCEIDHFFCDLPPL 190

Qy        185 IKLACTDT-------YLTGILIVTNSGTISLSCFLAVVTSYMVILVS-LRKHSAEGRQKA 236
              : ||| ||       ::  :| ::       | || :: ||: ||:: |   | ||| ||
Db        191 LALACGDTSQNEAAIFVVAVLCIS-------SPFLLIIYSYVKILIAVLLMPSPEGRHKA 243

Qy        237 LSTCSAHFMVVALFFGPCIFIYTRPDTSFS--IDKVVSVFYTVVTPLLNPFIYTLRNEEV 294
              |||||:| :|| ||:|     | || :| |  :|| :::|||||| :||| ||:|||:||
Db        244 LSTCSSHLLVVTLFYGSACITYLRPKSSHSPGMDKFLALFYTVVTSMLNPIIYSLRNKEV 303

Qy        295 KSAMKQ 300
              |:|:::
Db        304 KAALRR 309


RESULT 7
US-08-748-506-20
; Sequence 20, Application US/08748506
; Patent No. 6159707
;  GENERAL INFORMATION:
;    APPLICANT:  Ronnett et al.
;    TITLE OF INVENTION:  NOVEL SPERM RECEPTORS
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Leydig, Voit & Mayer, Ltd.
;      STREET:  Two Prudential Plaza, Suite 4900
;      CITY:  Chicago
;      STATE:  IL
;      COUNTRY:  US
;      ZIP:  60601-6780
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/748,506
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/033,751
;      FILING DATE:  09-NOV-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      REFERENCE/DOCKET NUMBER:  74940
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-616-5600
;      TELEFAX:  312-616-5700
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  321 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
US-08-748-506-20

  Query Match             39.0%;  Score 628.5;  DB 3;  Length 321;
  Best Local Similarity   43.5%;  Pred. No. 1.1e-45;
  Matches  130;  Conservative   56;  Mismatches  110;  Indels    3;  Gaps    2;

Qy          5 NQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMYFFLS 64
              |   |  | |   ::      | |     :::::|:|||| :|   :||||||||||:
Db         11 NSLSVKRFAFAKFSEVPGECFLLFTLILLMFLVSLTGNILIALAICTSPSLHTPMYFFLA 70

Qy         65 NLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAYDRYV 124
              ||| ::| ::   :||||: |: | : ||:: | :|:||   |   |  ||  :|:|||:
Db         71 NLSLLEIGYTCSVIPKMLQSLVSEARGISWEGCASQMFFFIFFGITECCLLAAMAFDRYM 130

Qy        125 AICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCDVPLV 184
              |||:||||   |:  ||  |    ]: | :  ||||     | :|||  || :|||:| :
Db        131 AICSPLHYATRMSRGVCAYLAIVSWVMGCIVGLGQTNFIFSLNFCGPCEIDHFFCDLPPL 190
```

```
Qy        185 IKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVS-LRKHSAEGRQKALSTCSAH 243
              : ||| ||       |  :     | || :::||: |||: |   | ||| |||||||:|
Db        191 LALACGDTSQNEAAIFVAAVLCIFSPFLLIISSYVRILVAVLVMPSPEGRHKALSTCSSH 250

Qy        244 FMVVALFFGPCIFIYTRPDTSFS--IDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300
               :|| ||:|     | |  :| |  :||::::||| || :|:| ||:|||:||| |:::
Db        251 LLVVTLFYGSTSATYLRSKSSHSPGVDKLLALFYTSVTSMLNPIIYSLRNKEVKGALRR 309


RESULT 8
US-08-748-506-19
; Sequence 19, Application US/08748506
; Patent No. 6159707
;  GENERAL INFORMATION:
;    APPLICANT:  Ronnett et al.
;    TITLE OF INVENTION:  NOVEL SPERM RECEPTORS
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Leydig, Voit & Mayer, Ltd.
;      STREET:  Two Prudential Plaza, Suite 4900
;      CITY:  Chicago
;      STATE:  IL
;      COUNTRY:  US
;      ZIP:  60601-6780
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/748,506
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/033,751
;      FILING DATE:  09-NOV-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      REFERENCE/DOCKET NUMBER:  74940
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-616-5600
;      TELEFAX:  312-616-5700
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  321 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
US-08-748-506-19

  Query Match             38.9%;  Score 626.5;  DB 3;  Length 321;
  Best Local Similarity   43.1%;  Pred. No. 1.6e-45;
  Matches  132;  Conservative   56;  Mismatches  101;  Indels   17;  Gaps    4;

Qy          5 NQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMYFFLS 64
              |   |  | |   ::      | |     :::::|:|| || :|   :|||||||||||:
Db         11 NSLSVKRFAFAKFSEVPGECFLLFTLILLMFLVSLTGNALIALAACTSPSLHTPMYFFLA 70

Qy         65 NLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAYDRYV 124
              ||| ::| ::   :|||: |: | : || : | ||:||    |   |  ||  :|:|| :
Db         71 NLSLLEIGYTCSVIPKMLQSLVSEAREISREGCATQMFFFTFFGITECCLLAAMAFDRCM 130

Qy        125 AICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCDVPLV 184
              ||:|||   |:  ||  |   | | :  ||||   | | :|||  || :|||:| :
Db        131 GICSPLHYATRMSREVCAHLAIVSWGMGCIVGLGQTNNIISLNFCGPCEIDHFFCDLPPL 190

Qy        185 IKLACTDT-------YLTGILIVTNSGTISLSCFLAVVTSYMVILVS-LRKHSAEGRQKA 236
              : ||| ||       ::  || ::       | || :: ||: |||: |   | ||| ||
Db        191 LALACGDTSQNEAAIFVAAILCIS-------SPFLVILYSYVRILVAVLVMPSPEGRHKA 243

Qy        237 LSTCSAHFMVVALFFGPCIFIYTRPDTSFS--IDKVVSVFYTVVTPLLNPFIYTLRNEEV 294
              |||||:| :|| ||:|   | | || :| |  :||::::||| || :||| ||:|||:||
Db        244 LSTCSSHLLVVTLFYGSVSFTYLRPKSSHSPGMDKLLALFYTAVTSMLNPIIYSLRNKEV 303

Qy        295 KSAMKQ 300
              |:|:::
Db        304 KAALRR 309


RESULT 9
US-08-748-506-11
; Sequence 11, Application US/08748506
; Patent No. 6159707
;  GENERAL INFORMATION:
;    APPLICANT:  Ronnett et al.
;    TITLE OF INVENTION:  NOVEL SPERM RECEPTORS
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Leydig, Voit & Mayer, Ltd.
;      STREET:  Two Prudential Plaza, Suite 4900
;      CITY:  Chicago
;      STATE:  IL
;      COUNTRY:  US
;      ZIP:  60601-6780
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/748,506
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/033,751
;      FILING DATE:  09-NOV-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      REFERENCE/DOCKET NUMBER:  74940
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-616-5600
;      TELEFAX:  312-616-5700
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  321 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-748-506-11

  Query Match             38.7%;  Score 623.5;  DB 3;  Length 321;
  Best Local Similarity   42.8%;  Pred. No. 2.9e-45;
  Matches  131;  Conservative   56;  Mismatches  102;  Indels   17;  Gaps    4;

Qy          5 NQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMYFFLS 64
              |   |  | |   ::      | |     :::::|:|| || :|   :|||||||||||:
Db         11 NSLSVKRFAFAKFSEVPGECFLLFTLILLMFLVSLTGNALIALAXCTSPSLHTPMYFFLA 70

Qy         65 NLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAYDRYV 124
              ||| ::| ::   :|||: |: | : || : | ||:||    |   |  ||  :|:|| :
Db         71 NLSLLEIGYTCSVIPKMLQSLVSEAREISREGCATQMFFFTFFGITECCLLAAMAFDRCM 130

Qy        125 AICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCDVPLV 184
              ||:|||   |:  ||  |   | | :  ||||   | | :|||  || :|||:| :
Db        131 GICSPLHYATRMSREVCAHLAIVSWGMGCIVGLGQTNXIXSLNFCGPCEIDHFFCDLPPL 190

Qy        185 IKLACTDT-------YLTGILIVTNSGTISLSCFLAVVTSYMVILVS-LRKHSAEGRQKA 236
              : ||| ||       ::  || ::       | || :: ||: |||: |   | ||| ||
Db        191 LALACGDTSQNEAAIFVAAILCIS-------SPFLVILYSYVRILVAVLVMPSPEGRHKA 243

Qy        237 LSTCSAHFMVVALFFGPCIFIYTRPDTSFS--IDKVVSVFYTVVTPLLNPFIYTLRNEEV 294
              |||||:| :|| ||:|   | | || :| |  :||::::||| || :||| ||:|||:||
Db        244 LSTCSSHLLVVTLFYGSVSFTYLRPKSSHSPGMDKLLALFYTAVTSMLNPIIYSLRNKEV 303
```

```
Qy        295 KSAMKQ 300
              |:|:::
Db        304 KAALRR 309


RESULT 10
US-08-748-506-12
; Sequence 12, Application US/08748506
; Patent No. 6159707
;  GENERAL INFORMATION:
;    APPLICANT:  Ronnett et al.
;    TITLE OF INVENTION:  NOVEL SPERM RECEPTORS
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Leydig, Voit & Mayer, Ltd.
;      STREET:  Two Prudential Plaza, Suite 4900
;      CITY:  Chicago
;      STATE:  IL
;      COUNTRY:  US
;      ZIP:  60601-6780
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/748,506
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/033,751
;      FILING DATE:  09-NOV-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      REFERENCE/DOCKET NUMBER:  74940
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-616-5600
;      TELEFAX:  312-616-5700
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  321 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-748-506-12

  Query Match             38.7%;  Score 623.5;  DB 3;  Length 321;
  Best Local Similarity   43.1%;  Pred. No. 2.9e-45;
  Matches  129;  Conservative   56;  Mismatches  111;  Indels    3;  Gaps    2;

Qy          5 NQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMYFFLS 64
              |  |  | |   ::      | |     :::::|:|| || :|   :||||||||||:
Db         11 NSLSVKRFAFAKFSEVPGECFLLFTLILLMFLVSLTGNTLIALAICTSPSLHTPMYFFLA 70

Qy         65 NLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAYDRYV 124
              ||| ::| ::   :||||: |: | : ||:: | :|:||   |   | ||  :|:|||:
Db         71 NLSLLEIGYTCSVIPKMLQSLVSEARGISWEGCASQMFFFIFFGITECCLLAAMAFDRYM 130

Qy        125 AICTPLHYPNVVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCDVPLV 184
              |||:||||   |:  ||  |    |: | :  ||||     | :|||  || :|||:| :
Db        131 AICSPLHYATRMSRGVCAYLAIVSWVMGCIVGLGQTNFIFSLNFCGPCEIDHFFCDLPPL 190

Qy        185 IKLACTDTYLTGILIVTNSGTISLSCFLAVVTSYMVILVS-LRKHSAEGRQKALSTCSAH 243
              : ||| ||      |  :     | || :::||: |||: |   | ||| |||||||:|
Db        191 LALACGDTSQNEAAIFVAAVLCIFSPFLLIISSYVRILVAVLVMPSPEGRHKALSTCSSH 250

Qy        244 FMVVALFFGPCIFIYTRPDTSFS--IDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300
               :|| ||:|     | |  :| |  :||:::|||  || :||| ||:|||:||| |:::
Db        251 LLVVTLFYGSTSATYLRSKSSHSPGVDKLLALFYTSVTSMLNPIIYSLRNKEVKGALRR 309


RESULT 11
US-08-748-506-13
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```
; Sequence 13, Application US/08748506
; Patent No. 6159707
;  GENERAL INFORMATION:
;    APPLICANT:  Ronnett et al.
;    TITLE OF INVENTION:  NOVEL SPERM RECEPTORS
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Leydig, Voit & Mayer, Ltd.
;      STREET:  Two Prudential Plaza, Suite 4900
;      CITY:  Chicago
;      STATE:  IL
;      COUNTRY:  US
;      ZIP:  60601-6780
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/748,506
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/033,751
;      FILING DATE:  09-NOV-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      REFERENCE/DOCKET NUMBER:  74940
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-616-5600
;      TELEFAX:  312-616-5700
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  321 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-748-506-13

  Query Match             38.3%;  Score 617.5;  DB 3;  Length 321;
  Best Local Similarity   42.0%;  Pred. No. 9.3e-45;
  Matches  129;  Conservative   59;  Mismatches  102;  Indels   17;  Gaps    4;

Qy          5 NQTRVTEFVFLGLTDNRVLEMLFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMYFFLS 64
              |  |  | |   ::      | |     :::::|:|| || :|   :||||||||||:
Db         11 NSLSVKRFAFAKFSEVPGECFLLFTLILLMFLVSLTGNALIALAICTSPSLHTPMYFFLA 70

Qy         65 NLSFIDICHSSVTVPKMLEGLLLERKTISFDNCITQLFFLHLFACAEIFLLIIVAYDRYV 124
              ||| ::| ::   :||||: |: | : |    | ||:||   |   | ||  :|:|||:
Db         71 NLSLLEIGYTCSVIPKMLQSLVSEAREIFQVGCATQMFFFIFFGITECCLLAAMAFDRYM 130

Qy        125 AICTPLHYPNVMNMRVCIQLVFALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCDVPLV 184
              |||:||||   |:  ||  |    |: | :  ||||     | :|||  || :|||:| :
Db        131 AICSPLHYATRMSREVCAHLAIVSWVMGCIVGLGQTNFIFSLNFCGPCEIDHFFCDLPPL 190

Qy        185 IKLACTDT-------YLTGILIVTNSGTISLSCFLAVVTSYMVILVS-LRKHSAEGRQKA 236
              : ||| ||       |  :  :| ::       | || :: ||: |||: |   | ||| ||
Db        191 LALACGDTSQIEAAIFVVVVLCIS-------SPFLLIIYSYVRILVAVLVMPSPEGRHKA 243

Qy        237 LSTCSAHFMVVALFFGPCIFIYTRPDTSFS--IDKVVSVFYTVVTPLLNPFIYTLRNEEV 294
              |||||:| :|| ||:|     | || :| |  :||:::||| || :||| ||:|||::|
Db        244 LSTCSSHLLVVTLFYGSGSVTYLRPKSSHSPGMDKLLALFYTAVTSMLNPIIYSLRNKDV 303

Qy        295 KSAMKQL 301
              |:|::::
Db        304 KAALRRI 310


RESULT 12
US-08-118-270-61
; Sequence 61, Application US/08118270
; Patent No. 5508384
```

```
;  GENERAL INFORMATION:
;    APPLICANT:  Murphy, Randall B.
;    APPLICANT:  Schuster, David I.
;    TITLE OF INVENTION:  POLYPEPTIDES OF G-COUPLED PROTEIN
;    TITLE OF INVENTION:  RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
;    NUMBER OF SEQUENCES:  348
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/118,270
;      FILING DATE:  09-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/943,236
;      FILING DATE:  10-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Townsend, Kevin G.
;      REGISTRATION NUMBER:  34,033
;      REFERENCE/DOCKET NUMBER:  MURPHY=2A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;      TELEX:  248633
;  INFORMATION FOR SEQ ID NO:  61:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  284 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-118-270-61

  Query Match             37.2%;  Score 599.5;  DB 1;  Length 284;
  Best Local Similarity   41.9%;  Pred. No. 2.7e-43;
  Matches  117;  Conservative   61;  Mismatches   94;  Indels    7;  Gaps    4;

Qy         26 LFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMYFFLSNLSFIDICHSSVTVPKMLEGL 85
              | |: |  :|: |: ||:|||:|      |||||||||||||:|:| || ||||:|
Db          1 LLFLLFLIMYLATVLGNLLIILAIGGDSRLHTPMYFFLSNLSFVDVCFSSTTVPKVLANH 60

Qy         86 LLERKTISFDNCITQLFFLHLFACAEIFLLIIVAYDRYVAICTPLHYPNVMNMRVCIQLV 145
              :|  : |||  |:|||:|| :|   : ||| :::|||||||| |||| :   ::|: ||
Db         61 ILGSQAISFSGCLTQLYFLAVFGNMDNFLLAVMSYDRYVAICHPLHYTTI--RQLCVLLV 118

Qy        146 FALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCDVPLVIKLACTDTYLTGILIVTNSGT 205
              |:   :: |     :  |  :|     :  :|||   ::||:|:||:|  ::|:|
Db        119 VGSWVVANMNCLLHILIMARKSFCAD--LPHFFCDGTPLLKLSCSDTHLNELMILTEGAV 176

Qy        206 ISLSCFLAVVTSYMVILVS-LRKHSAEGRQKALSTCSAHFMVVALFFGPCIFIYTRPDTS 264
              : :: |: :: ||: |  : ||  |  |  |: ||| :|  || ||:|  | :|  | :|
Db        177 VMVTPFVCILISYIHITCAVLRVSSPRGGWKSFSTCGSHIAVVCLFYGTVIAVYFNPSSS 236

Qy        265 F--SIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQL 301
                 |   :| | ||||::|||||:||| ::|:|:::::
Db        237 HLAGRDMAAAVMYAVVTPMINPFIYSLRNSDMKAALRKV 275


RESULT 13
PCT-US93-08528-61
; Sequence 61, Application PC/TUS9308528
;  GENERAL INFORMATION:
;    APPLICANT:  New York University
;    TITLE OF INVENTION:  POLYPEPTIDES OF G-COUPLED PROTEIN
;    TITLE OF INVENTION:  RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
;    NUMBER OF SEQUENCES:  348
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/08528
;      FILING DATE:  09-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/943,236
;      FILING DATE:  10-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Townsend, Kevin G.
;      REGISTRATION NUMBER:  34,033
;      REFERENCE/DOCKET NUMBER:  MURPHY=2 PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;      TELEX:  248633
;  INFORMATION FOR SEQ ID NO:  61:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  284 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
PCT-US93-08528-61

  Query Match             37.2%;  Score 599.5;  DB 5;  Length 284;
  Best Local Similarity   41.9%;  Pred. No. 2.7e-43;
  Matches  117;  Conservative   61;  Mismatches   94;  Indels    7;  Gaps    4;

Qy         26 LFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMYFFLSNLSFIDICHSSVTVPKMLEGL 85
              | |: |  :|: |: ||:|||:|      |||||||||||||:|:| || ||||:|
Db          1 LLFLLFLIMYLATVLGNLLIILAIGGDSRLHTPMYFFLSNLSFVDVCFSSTTVPKVLANH 60

Qy         86 LLERKTISFDNCITQLFFLHLFACAEIFLLIIVAYDRYVAICTPLHYPNVMNMRVCIQLV 145
              :|  : |||  |:|||:|| :|   : ||| :::|||||||| |||| :   ::|: ||
Db         61 ILGSQAISFSGCLTQLYFLAVFGNMDNFLLAVMSYDRYVAICHPLHYTTI--RQLCVLLV 118

Qy        146 FALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCDVPLVIKLACTDTYLTGILIVTNSGT 205
              |:   :: |     :  |  :|     :  :|||   ::||:|:||:|  ::|:|
Db        119 VGSWVVANMNCLLHILIMARKSFCAD--LPHFFCDGTPLLKLSCSDTHLNELMILTEGAV 176

Qy        206 ISLSCFLAVVTSYMVILVS-LRKHSAEGRQKALSTCSAHFMVVALFFGPCIFIYTRPDTS 264
              : :: |: :: ||: |  : ||  |  |  |: ||| :|  || ||:|  | :|  | :|
Db        177 VMVTPFVCILISYIHITCAVLRVSSPRGGWKSFSTCGSHIAVVCLFYGTVIAVYFNPSSS 236

Qy        265 F--SIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQL 301
                 |   :| | ||||::|||||:||| ::|:|:::::
Db        237 HLAGRDMAAAVMYAVVTPMINPFIYSLRNSDMKAALRKV 275


RESULT 14
US-08-118-270-60
; Sequence 60, Application US/08118270
; Patent No. 5508384
;  GENERAL INFORMATION:
;    APPLICANT:  Murphy, Randall B.
;    APPLICANT:  Schuster, David I.
;    TITLE OF INVENTION:  POLYPEPTIDES OF G-COUPLED PROTEIN
;    TITLE OF INVENTION:  RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
;    NUMBER OF SEQUENCES:  348
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
```

```
;       STREET:  419 Seventh Street, N.W., Suite 300
;       CITY:  Washington
;       STATE:  D.C.
;       COUNTRY:  USA
;       ZIP:  20004
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/118,270
;       FILING DATE:  09-SEP-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/943,236
;       FILING DATE:  10-SEP-1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Townsend, Kevin G.
;       REGISTRATION NUMBER:  34,033
;       REFERENCE/DOCKET NUMBER:  MURPHY=2A
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-628-5197
;       TELEFAX:  202-737-3528
;       TELEX:  248633
;   INFORMATION FOR SEQ ID NO:  60:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  293 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-118-270-60

  Query Match             35.6%;  Score 573;  DB 1;  Length 293;
  Best Local Similarity   42.2%;  Pred. No. 4.8e-41;
  Matches  116;  Conservative   52;  Mismatches   95;  Indels   12;  Gaps    3;

Qy         26 LFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMYFFLSNLSFIDICHSSVTVPKMLEGL 85
                |  :  | ::|::|: ||| ||:| :  | ||||||||||||||:|||  | |||   :
Db          1 LIYGLFLSMYLVTVIGNISIIVAIISDPCLHTPMYFFLSNLSFVDICFISTTVPVNTQ-- 58

Qy         86 LLERKTISFDNCITQLFFLHLFACAEIFLLIIVAYDRYVAICTPLHYPNVMNMRVCIQLV 145
                 :   |::  |||||::|  ||   : ||| |:|||||||| |:||  :|| ::|  ||
Db         59 -TQNNVITYAGCITQIYFFLLFVELDNFLLTIMAYDRYVAICHPMHYTVIMNYKLCGFLV 117

Qy        146 FALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCDVPLVIKLACTDTYLTGILIVTNSGT 205
               |:   :|:|   | :: ||:|    |  |||:   ||:| |:| :|  ::|
Db        118 LVSWIVSVLHAL---FQSLALPFCTHLEIPHYFCEPNQVIQLTCSDAFLNDLVIYFTLVL 174

Qy        206 ISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTCSAHFMVVALFFGPCIFIYTRPDTSF 265
               ::      :  ||  |       |  |: || |||::|  ||:||:   : :|     :
Db        175 LATVPIAGIFYSYFAI------SSVHGKYKAFSTCASHLSVVSLFYCTGLGVYLSSAANN 228

Qy        266 SIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300
               |:    || ||||||::|||||:|||::||| :|:
Db        229 SLSATASVMYTVVTPMVNPFIYSLRNKDVKSVLKK 263


RESULT 15
PCT-US93-08528-60
; Sequence 60, Application PC/TUS9308528
;  GENERAL INFORMATION:
;    APPLICANT:  New York University
;    TITLE OF INVENTION:  POLYPEPTIDES OF G-COUPLED PROTEIN
;    TITLE OF INVENTION:  RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
;    NUMBER OF SEQUENCES:  348
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/08528
;      FILING DATE:  09-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/943,236
;      FILING DATE:  10-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Townsend, Kevin G.
;      REGISTRATION NUMBER:  34,033
;      REFERENCE/DOCKET NUMBER:  MURPHY=2 PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;      TELEX:  248633
;  INFORMATION FOR SEQ ID NO:  60:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  293 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
PCT-US93-08528-60

  Query Match             35.6%;  Score 573;  DB 5;  Length 293;
  Best Local Similarity   42.2%;  Pred. No. 4.8e-41;
  Matches  116;  Conservative   52;  Mismatches   95;  Indels   12;  Gaps    3;

Qy         26 LFFMAFSAIYMLTLSGNILIIIATVFTPSLHTPMYFFLSNLSFIDICHSSVTVPKMLEGL 85
                |  :  | ::|::|: ||| ||:| :  | ||||||||||||||:|||  | |||   :
Db          1 LIYGLFLSMYLVTVIGNISIIVAIISDPCLHTPMYFFLSNLSFVDICFISTTVPVNTQ-- 58

Qy         86 LLERKTISFDNCITQLFFLHLFACAEIFLLIIVAYDRYVAICTPLHYPNVMNMRVCIQLV 145
                 :   |::  |||||::|  ||   : ||| |:|||||||| |:||  :|| ::|  ||
Db         59 -TQNNVITYAGCITQIYFFLLFVELDNFLLTIMAYDRYVAICHPMHYTVIMNYKLCGFLV 117

Qy        146 FALWLGGTVHSLGQTFLTIRLPYCGPNIIDSYFCDVPLVIKLACTDTYLTGILIVTNSGT 205
               |:   :|:|   | :: ||:|    |  |||:   ||:| |:| :|  ::|
Db        118 LVSWIVSVLHAL---FQSLALPFCTHLEIPHYFCEPNQVIQLTCSDAFLNDLVIYFTLVL 174

Qy        206 ISLSCFLAVVTSYMVILVSLRKHSAEGRQKALSTCSAHFMVVALFFGPCIFIYTRPDTSF 265
               ::      :  ||  |       |  |: || |||::|  ||:||:   : :|     :
Db        175 LATVPIAGIFYSYFAI------SSVHGKYKAFSTCASHLSVVSLFYCTGLGVYLSSAANN 228

Qy        266 SIDKVVSVFYTVVTPLLNPFIYTLRNEEVKSAMKQ 300
               |:    || ||||||::|||||:|||::||| :|:
Db        229 SLSATASVMYTVVTPMVNPFIYSLRNKDVKSVLKK 263


Search completed: August 12, 2003, 16:10:23
Job time : 31 secs
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